



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 173593

TO: Sean McGarry
Art Unit: 1635
Location: REM/2D19/2C18
Serial Number: 09/913858

Monday, February 27, 2006

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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McGarry, S.
09/19/3858 Page 1
Seq. ID 1

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2006, 15:34:03 ; Search time 10739 Seconds
(without alignments)
11634.408 Million cell updates/sec

Title: US-09-913-858C-1
Perfect score: 2198
Sequence: 1 actaactcaaacgtgcatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sv.*
12: gb_un.*
13: gb_vi.*
14: gb_hcg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		Description	
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4	1078.6	49.1	2027	15	AY082444	Medicago	
5	1068.2	48.6	2134	15	AY082445	Medicago	
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ALIGNMENTS

RESULT 1
BD270213
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD270213
Alpha 1,3-fucosyltransferase r36247.
BD270213
BD270213.1 GI:33079981
JP 2002536978-A/1.
unidentified
unclassified
unclassified
Altmann, F.
Alpha 1,3-fucosyltransferase r36247
Patent: JP 2002536978-A 1 05-NOV-2002;
FRIEDRICH ALTMANN
OS Unknown
PN JP 2002536978-A/1
PD 05-NOV-2002
PP 17-FEB-2000 JP 2000599878
PR 18-FEB-1999 AT A 270/99
PI FRIEDRICH ALTMANN
PC C12N15/09,A01H5/00,A01K67/033,A61K38/45,A61P37/08,
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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 ACCESSION AY082444
 VERSION AY082444.1 GI:37543455
 KEYWORDS
 SOURCE Medicago sativa
 ORGANISM Medicago sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE
 1 (bases 1 to 2027)
 SOURCILE, C., Kiefer-Meyer, M.-C., Faye, L. and Gomord, V.
 Direct Submission
 Submitted (06-MAR-2002) LTI-CNRS UMR6037, Universite de Rouen, Bat. Extension Biologie, Mont Saint Aignan 76821, France

FEATURES
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 Query Match 49.1%; Best Local Similarity 77.2%; Pred. No. 1.7e-252;
 Matches 1405; Conservative 0; Mismatches 374; Indels 42; Gaps 6;

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 244 AGAAGATGATGTCGCCAACAGACAGCTTACCGCTTTTGGCTCGGGGAGGCAACCCAAAG 303
 232 ACAACCCAAAGAGGTTTACCAG-----TTTTCAGTTTTCAGTTTCAACAACGTTCCGAA 285

QY	304	AGGAAATGGAGCAATCTAATGCTCTTGTGTGTCCTTGTGTGCTCATCGCGAGATCGCG	363
Db	286	AAGAAATGGTCGAATTTAATGCCCTTTATTGTAGCACCTTGTGGTTATTGGGAGATCGCG	345
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QY	838	ATGGCACCAAGTCAAGCGGAAACTGAACTGCTGCTTGCAGCTGCTTTTCCAAATTCGT	897
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QY	1897	ACACTTTAAATTTAAACTTGTTCGTAGAAGTGCAAAATCCCATATTTATATGCTTAGTTT	1956
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RESULT 5			
AY082445			
LOCUS			
DEFINITION	Medicago sativa clone MS1-3Ftb alpha 1,3 fucosyltransferase mRNA,	2134 bp	linear
ACCESSION	AY082445		
VERSION	AY082445.1	GI:37543463	
KEYWORDS			
SOURCE	Medicago sativa		
ORGANISM	Medicago sativa		
REFERENCE	1 (bases 1 to 2134)		
AUTHORS	Sourrouille,C., Kiefer-Meyer,M.-C., Faye,L. and Gomord,V.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-MAR-2002) LTI-CNRS UMR6037, Universite de Rouen, Bat.		
EXTENSION	Biologie, Mont Saint Aignan 76821, France		
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ORIGIN

Query Match		48.6%; Score 1068.2; DB 15; Length 2134;
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Matches 1393; Conservative 0; Mismatches 383; Indels 45; Gaps 5;		
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Qy	364	TTCTCGGTGAGTTCGATATGSCAAAACGCCGATGGTTGACTCCCTCGCTGACTTC 423
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Qy	658	GCAATTTGGTTACCTCAACAGTGGAAACAGCTAGCATTCCTCGATCAATGAATCAGGA 717
Db	637	GCAATTTGGCTTACCTCAGCAAGCTGGAACAGCAAGTGTCTGAGATCAATGGAGTCGGA 696
Qy	718	GAATACTATGCTGAGAACAAATATGCCATGGCAAGCAGGAGGGGATATAACATCGTAATG 777
Db	697	CAATACTATGCAAGAACAAATCTTGGCATGGCAGCAGGAGGGGATATCACATTTGTAATG 756
Qy	778	ACAAACAGTCTATCTTCGGATGTTCTGTGTGGATATTTTTTCATGGGCTGAGTATGATG 837
Db	757	ACAAACAGTCTATCATCTGACGCTCCTGTGGATATTTTTTCATGGGCTGAGTATGACATC 816
Qy	838	ATGGCAACAGTGCAGCCGAAAACCTGAAGCTGCTCTTGGAGCTGCTTTCATTTCCAAATGT 897
Db	817	ATGGCAACGATAAAGCCAAAACCTGAAAAGCTCTTGCAGCTGCTTTTATTTTCCAAATGT 876
Qy	898	GCTGCTCGAAATTTCCGGTTGCAAGCTCTTGGCCCTTGGAGGCTTGAATAACCAATCAAAAT 957
Db	877	GCTGCTCGAAATTTCCGATTTGAAGCTCTGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGA 936
Qy	958	GATTTCTTATGGTGGTGTGACAGGAACCGTGTATGGAAGAGTGAAACAAAGTGGAGGCCCTG 1017
Db	937	GACTCTTATGGTAGTGTGATAGGAATCGTGTATGGAAGAGTGGACAAACCTGGAAACCTGTG 996

RESULT 6
AJ891040
LOCUS

Populus tremula x Populus alba mRNA linear
1569 bp
PLN 22-MAR-2005

DEFINITION
Populus tremula x Populus alba mRNA for alpha 1.3

Qy	1018	AAGCACTACAAATTTAGCTTTAGCGTTTGAATAATCGAATAGGGAAGATTATGTAACTGAA 1077
Db	997	ACGGCTACAAATTTAGCTTTAGCAATTTGAAATTTCTAACGAGGAGGATTATGTAACTGAA 1056
Qy	1078	AAATTTCTCAATCCCTTGTGCTGGAACGTCTCCCTGGTGGTGTGGTCTCCAAATATT 1137
Db	1057	AAGTTTTTCCAGTCGCTTGTGCTGGAACATATCCCTGGTGGTGTGGTCTCCAAATATT 1116
Qy	1138	CAGGACTTTGCTCTCTCTCTCTCTCTCAATTTTACATATTAAGAAGATAGAGGATGTTGAG 1197
Db	1117	CAAGATTTTGTCTCTCTCTCTCTCTCTCAATTTTATATATCAAGAAGATAGAGGATGTTGAG 1176
Qy	1198	TCTGTTGCAAGACCATGAGATATCTAGCAGAAAATCCGGAAGCATATAATCAATCATG 1257
Db	1177	TCTGTTGCCAAGTCCATGAGATACCTAGCAGAAAACCTCGAAGCATATAATCAATCATG 1236
Qy	1258	AGGTGGAAGTATGAGGTTCATCTGACTCTTCAAGGCCCTTGTGGATATGCGAGCTCG 1317
Db	1237	AGGTGGAAGTATGAGGGCCATCTGATTTCTTTCAAGCCCTTGTGGATATGCGAGCTGTA 1296
Qy	1318	CATTTCATCGTCCGCTCTTTTGCATTTTCACTTGGCCACAGTGAGTAGAGAGAAGGAGAAAAT 1377
Db	1297	CATTTCATCTTCCGCCCTTTGCTTCACTTGGCCACAAAGATAGAGAGAAGGAGAGAG 1356
Qy	1378	AATCCAAAGCCTTAAAGAGACGCTCTTGCAGAGTGCACTAGAGGGCCAGAAAACCGTATATCAT 1437
Db	1357	AGCCAGAGCTTCAAGAGAGCCTTGCAGGTGCACTCGAGGCTCAGAAAATGTAATCAT 1416
Qy	1438	ATCTATGTCAGAGAAAGGGGAGGTTTGAGATGAGAGTCCATTTACTGAGGCTTAGCAAT 1497
Db	1417	ATCTATGTCAGAGAAAGGGGAAACATTTGAGATGAGAGTCCATTTACTTGAGATCTAGCAAT 1476
Qy	1498	TTAACTCTGAATGCTGTGAAAGGCTGCTGTTGTTTGAAGTTTCACTCCCTGAATCTTGTG 1557
Db	1477	TTAACTCTGGAGTCTCTTCAAGAGTCTGTTCTTCAAGAGTTTCACTCCCTGAATCATGTT 1536
Qy	1558	CCTGTATGGAAGACGTGAAGGCTGAAAGTATTAAGAGGGGGAGTGTCTTAAACCTCTAC 1617
Db	1537	CCTGTATGGAAGCCTGAAAGACCTCAAATTTCTAAAGGTTGGCGATAAAATTTGAAGGTTTAC 1596
Qy	1618	AAATATATACCAATTTGGCTTGACACAGAGACAGCTCTTTTATACCTTCAGCTTCAAGGT 1677
Db	1597	AAATATATACCTTGGCGGCTTGACACAGAGGCAAGCTCTTTATACCTTCCAGTTCAACGG 1656
Qy	1678	GATGCTGATTTTCAAGAGTCACTTGGAGAACAACTCTGTGCCAAGTTTGAAGTCAATTTT 1737
Db	1657	GATGTTGATTTTCAAGAGTCACTTGGAAAGCAATCTCTGTGCCAAGTTTGAAGTCAATTTT 1716
Qy	1738	GTGTAGCATGGCTAA-----ATGGTACCTCTGCTCTACCTGAATTAGCTTCACTTAG 1790
Db	1717	GTGTAGCATATGTTGAGCTACCTACAAATTTACATGATCACCTAGCATTAGCTCTTTCAC 1776
Qy	1791	CTGAGCCTAGCTAGAGTTTGTAGGAATGAGTATGCGAGTGAATATGCGCATGCGCTT----- 1845
Db	1777	TAACTGAGAGAATGAATTTTAGGAATGAGTATGACCATGAGAGTGGAGTGGCATGTTGTA 1836
Qy	1846	-----TATTTATGCTAGTCTTTTGGCCAACTCATTTGATGTTTCTGTAAGACATC 1896
Db	1837	TGCCTTACCTTACTTTGGCCAACTCATTCGGGGATTTTACATTCAGAAAATATACATGACTTC 1896
Qy	1897	ACACTTTAATTTAAACTTGTTCCTGTAGAACTGCAAAATCCATATTTAATGCTTAGTTTT 1956
Db	1897	AACATCTTAAACCCCTTTTGTGAAGATACTGAATGTTTCATATTTAATGTTGGGTTAT 1956
Qy	1957	AGTGTCTTATCTGATCATCT 1977
Db	1957	AGTGTCTTATCTGATCAT 1977

ACCESSION	fucosyltransferase (poFUT2 gene), clone INRA 717 1B4.	
VERSION	AJ891040.1 GI:61845102	
KEYWORDS	alpha 1,3 fucosyltransferase; poFUT2 gene.	
SOURCE	Populus alba x Populus tremula	
ORGANISM	Populus alba x Populus tremula	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;	
	rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.	
REFERENCE	1	
AUTHORS	Labrousse, P., Lhernould, S. and Costa, G.	
TITLE	Complex N-glycan biosynthesis in poplar trees	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1569)	
AUTHORS	Costa, G.	
TITLE	Direct Submission	
JOURNAL	Submitted (21-MAR-2005) Costa G., Eq. de Glycobiologie Forestiere,	
	Faculte des Sciences et Techniques, 123, Avenue Albert Thomas,	
	87060, Limoges, FRANCE	
FEATURES	Location/Qualifiers	
source	1..1569	
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gene	1..1569	
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CDS	1..1569	
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	DAGFGLPQGGTASVLRSMESASYAENNIHARRGYDVMTTSLSDVPVGFYSWAE	
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	KVTLKRYKFLAFENEDYVTEKFFQSLVAGTI PVVVGAPNI ODPAFAPNSILHI	
	RKLEDVDSIAKTMKYLIGENPDAYNQSIRWKYEGPDSFKALVDMAAVHSSCRLCILA	
	TMIREKEBNSPGFKRCPKCTDLETVVHLVYPERGRFQMESIFLRSGNLTVNALFAA	
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ORIGIN		
Query Match	38.1%; Score 837.2; DB 15; Length 1569;	
Best Local Similarity	74.9%; Pred. No. 1.8e-193;	
Matches 1097; Conservative	0; Mismatches 343; Indels 24; Gaps 3;	
QY	301 AAGAGGAAATGGAGCAATCTAATGCGCTCTTGTGTGTCCTTGTGTGTCATCGCGGAGATC	360
DB	109 AAAATGAAGTGGTCAAAATTTTGGCCAAATTTTGTGCTCTCTGTGTGTATGACAGATC	168
QY	361 GCGTTTCTGGGTAGTGGATATGGCCAAAACCGCCGCGATGGTGAATCCCTCGCTGAC	420
DB	169 GCCTTTCTGGGTGCTCTGTATATGGCTTAAATATGCGGATTTAGTATTCTGGGCTGAT	228
QY	421 TTCTTCTACCGC-----TCTCGAGCGGTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGA	468
DB	229 AGTTTTTCTACAGGTCAACTATATCTGCTGATATGTTGGAAGTGAAGTGAAGTGAAGTGA	288
QY	469 G-----GTTTGGTGGCTCTGATCGGAAATTCGAATCGTATAGTTGTGAGGAAATGG	519
DB	289 GAAACAGTGAATATGGATAAACTAATGGAATCTCGAGTCAGATAGTGTGAGGAGTGG	348
QY	520 TTGGAGGAGGAGATGCTGTGACGTATTCCAGGGGCTTTTCCAAAGAGCCTATTTTGT	579
DB	349 TTGAAAAGGAGGATGCTGTGGTTATTTCAGAGATTTTGTATAAAGACCCCGTTTGGTC	408
QY	580 TCTGGAGCTGATCAGGAGTGAAGTCTGTTTCGTTGATGTAATTTTGGTTTATAGTGG	639

DB	409 GCTGGAGCGGAAAGAGGTGGAACACATGCTGGGGTGAATGTTCAGTTTGGATTTAAACCCC	458
QY	640 GATAGAAAGCCAGATGCCGCCATTTGGGTATACCTCAACCAAGTGGAAACAGCTAGCATCTG	699
DB	469 AGTAAGAAGCCAGATGCTGGATTTGGCTTACCTCAACCAAGTGGAAACAGCTAGTGTGTTA	528
QY	700 CGATCAATCGAATCAGCAGAACTACTATGCTGAGAGAACTATTTGCCATGCTCAACAGCGAGG	759
DB	529 AGGTGATGGAATCAGCTTCTTACTATGAGAGAACTATTTGCTCAGGACGAC--GG	585
QY	760 GGATATAACATCGTAAATGACCAACCACTCTATCTCGGATGTTCTCTGTGGATATTTTCA	819
DB	586 GGATATGATGTTGTAATGACACGAGTCTCTCTCAGATGTGCCAGTTGGATATTTTCC	645
QY	820 TGGGCTGAGTATGATATGATGGACCAAGTCAGCGCGAAACCTGAAGCTGCTCTTCAGCT	879
DB	646 TGGGCTGAGTATGATATGATGGACCAAGTCAGCGCGAAACCTGAAGCTGCTCTTCGCT	705
QY	880 GCTTTCAATTTCCAAATTTGCTGCTCGAAATTTCCGGTTCCAAAGCTCTTGAGGCGCTTGAA	939
DB	706 GCTTTCAATTTCCAAATTTGCTGCTCGAAATTTCCGGTTCCAAAGCTCTTGAGCTTGAA	765
QY	940 AAATCAAAACATCAAAATTTGATTTCTTATGCTGTTGTCACAGGAACCGTGATGAAAGTG	999
DB	766 AGGTTGAACATCAACATAGATTTCTTATGCTAACTGCCATCGGAACCATGACGGAAGTG	825
QY	1000 AACAAAGTGAAGCCCTGAAGCACTACAAATTTAGCTTAGCTTGAAGCTTGAAGCTTGAAGT	1059
DB	826 GATAAAGTAAAGACTCTGAAGCGTTTACAAATTTAGCTTGGCTTTGAGAATTTCCAATGAG	885
QY	1060 GAAGATTATGAATGAAATTTCTTCAATCCCTTGTGCTGGAACCTGCTGCTGCTGTT	1119
DB	886 GAGGATTATGTCAGAGAAATTTCTTCAATCTTGTGCTGGAACCATACCTGCTGCTGTA	945
QY	1120 GTTGTGCTCCAAATATTCAGGACTTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1179
DB	946 GTTGTGCTCCAAATATTCAGGACTTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1005
QY	1180 GAGATAGAGATGTTGAGTCTGTTGCAAGACCATGAGATATCTAGCAGAAATCCCGAA	1239
DB	1006 AAGTAGAAGATGTTGATTTCAATTTGCAAGACATATGAAATACCTTTGAGAGAAATCTCGAT	1065
QY	1240 GCATATAATCAATCATTTGAGGTGGAATGAGGTGCTCACTGACCTCTTCAAGGCGCTT	1299
DB	1066 GCTTACATCAATCATTTAAGTGGAAATAGAGGGCCCATCTGATTTCTTCAAGGCACTG	1125
QY	1300 GTGGATATGGCAGCTGTGCAATTCATCGTCCGTCTTTTGCATTCATCTGGCCACAGTGAGT	1359
DB	1126 GTAGATATGGCAGCAGTACACTCATCATCGCGTCTTTTGCATTCACCTTGTACTATGATT	1185
QY	1360 AGAGAGAAGAGAAATTAATCCAAGCTTAAGAGACGCTCTTGAAGTGCACCTAGAGGG	1419
DB	1186 CGGAGAGAGAGAGAAATAGCCAGGGTTTAAAGAGCGTCCCTGCGAGATGCACAAAGAC	1245
QY	1420 CCAGAAACCGTATATCATATCTATGTCAGAGAAAGGGAGGTTTTCAGATGGAGTCCATT	1479
DB	1246 TTAGAGACCGTGTATCATTTATATGTAAGAGAGAGAGAGATTTTCAGATGGAGTCCATT	1305
QY	1480 TACTGAGGTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTTGTGAAGTTC	1539
DB	1306 TTCTTGAGGTCTGGCAATCTAACTGTAAATGCTCTAGAGGCTGCTGCTCAAGAGTGT	1365
QY	1540 ACATCCCTGAATCTGTGCTGTATGGAAGCTGAAGGCTGAAGTTATAAGAGGGGG	1599
DB	1366 AAGTCTTTGAAGCATGTGCCCATCTGGAAGCAGGAAAGACCTGAAAGCATAAAGGGAGGA	1425
QY	1600 AGTGTCTTTAAACTCTFACAAAATATATACCAATTTGGCTTGACACAGAGACAAGCTCTTTAT	1659
DB	1426 GAGCATTTTAAAGTTTACAGATATACCTGTAGGATGATGACACAGAGGCAAGCTCTGTAC	1485
QY	1660 ACCTTCAGCTTCAAGAGGTGATGCTGATTTTCAGGAGTCACTTGGAGAACAACTCTTGTGCC	1719

Db	1486	TCATTCAAACATGATGATGATTTCAAGAAATCACTTGGGAAGTCAACCCATGTGCA	1545
Qy	1720	AAGTTGAAGTCATTTTGTGTAG	1743
Db	1546	AAGTTGAGGTGATATTGTCTAG	1569
RESULT 7			
ATH404860			
LOCUS			
DEFINITION	Arabidopsis thaliana mRNA for alpha1,3-fucosyltransferase (FucTA gene).		
ACCESSION	AT404860		
VERSION	AJ404860.1	GI:13992482	
KEYWORDS	alpha 1,3-fucosyltransferase; FucTA gene.		
SOURCE	Arabidopsis thaliana (Chale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	Wilson, I.B., Rendic, D., Freilinger, A., Domic, J., Altmann, F., Mucha, J., Muller, S. and Hauser, M.T.		
TITLE	Cloning and expression of cDNAs encoding alpha1,3-fucosyltransferase homologues from Arabidopsis thaliana		
JOURNAL	Biochim. Biophys. Acta 1527 (1-2), 88-96 (2001)		
PUBMED	11420147		
REFERENCE	2 (bases 1 to 1506)		
AUTHORS	Wilson, I.B.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-JUL-2000) Wilson I.B.H., Institut fuer Chemie, Universitaet fuer Bodenkultur, Muthgasse 18, Wien 1190, Austria		
FEATURES	Location/Qualifiers		
source	1..1506		
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ORIGIN			
Query Match	31.4%	Score 690;	DB 15; Length 1506;
Best Local Similarity	72.0%	Pred. No. 1.8e-157;	
Matches 900;	Conservative 0;	Mismatches 350;	Indels 0; Gaps 0;
Qy	493	TCGTAATCGTAGTTGTGAGGAATGGTTGGAGAGGAGGAGTGTGTACGTATTTCGAGG	552
Db	256	TCAGGAATAGAAATGCCAGAGTGGTTAGAGAGTGGATTCACTTACTTATCTAGA	315
Qy	553	GGCTTTTCAAAGAGCCTATTTTGTCTCGAGCTGTATCAGAGTGGAAAGTCGTGTTCG	612
Db	316	GATTTCACTAAAGATCCGATTTTATCTCTGTGTAGTAAACAGGACTTCAATCGTGTCT	375
Qy	613	GTGGATGTAAATTTGGGTTTGTAGTGGGGATAGAAAGCCAGATGCCCATTTGGGTACCT	672

Db	376	GTGTAATGTGTAATGGGATTCACCTTCAGATAAGAAACCTGATCGGCTTTTGGATTAAGT	435
Qy	673	CAACCAAGTGGACAGCTAGCATTTCTCGCATCAATGGAATCAGCAGAAATCTACTGTCTGAG	732
Db	436	CATCAACCTGGAACTCAGTATAATCCGTTCAATGGAATCAGCAGTATTACCAAGAG	495
Qy	733	AACAATATTGCCATGCGCAAGACGAGGGGATATAACATCGTAATGACAAACAGTCTATCT	792
Db	496	AATAATCTTGCTCAAGCAGCAGCGAAAGGTTATGATATTGTGATGACAACTAGTCTGTCA	555
Qy	793	TCGGAATGTTCTGTGTGGATATTTTTCATGGCTGAGTATCATATGATGAGCCAGTCCAG	852
Db	556	TCAGATGTTCTGTGTGGTATTTTTCATGGCGGGAATATGATATTATGGGTCCAGTCCAA	615
Qy	853	CCGAAACTCAAGCTGCTCTTGAGCGCTTTTTCATTTTCAATTTGCTGTGCTCGAAATTTTC	912
Db	616	CCAAAAACAGAGAAAGCTCTTGCTGCTCTTTTATTTTCCAAATTCGCGCGCTCGGAATTC	675
Qy	913	CGGTTGCAAGCTCTTGAGGCGCTTTGAAAAATCAAAACATCAAAATTTGATTTTATGGTGT	972
Db	676	CGCTGCAAGCTCTTGAAGCTTTAATGAAGACGAATGTTAAGATTGATTTCTTATGGTGT	735
Qy	973	TGTCACAGAACCGTGTATGGAAGAGTGAAACAAAGTGAAGCCCTGAAGCAGTACAAATTT	1032
Db	736	TGTCACCGAATCGGATGGAGTGTGAGAGAGGTTGAAGCTCTTAAGCAGTACAAATTC	795
Qy	1033	AGCTTAGCGTTGAAATTCGAATGAGGAAGATTTATGTAATGAAAAATTTCTTCCAAATCC	1092
Db	796	AGCTAGCTTTTGAGAACACCAACGAGGAGGATTTATGTCAGAGAGAGTTCTTCCAAATCT	855
Qy	1093	CTTCTGCTCGAACTGTCCTCTGTTGTTGTTGCTCTCCAAATATTCAGGAGCTTTGCTCTCT	1152
Db	856	CTAGTCTGAGTCTGTCCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	915
Qy	1153	TCTCTCGTTCAATTTTACATATTAAGAGATAGAGAGTGTGAGTCTGTGTTGAAAGACC	1212
Db	916	TCTCTGACTCATTTCTTCAATTAAGCAGATGATGATGTCAGAGGAGGTTGTCAGAGAAA	975
Qy	1213	ATGAGATATCTAGCAGAAATCCCGAGCATATTAATCAATCATTTGAGTGAAGTATGAG	1272
Db	976	ATGAAGTATCTTGGCGATAACCCCTGACGCTTATTAATCAGCGCTAAGATGGAACATGAA	1035
Qy	1273	GGTCCATCTGACTCTTCAAGGCCCTTGTGATATGCGAGCTGTGCTATTCATCTGCGCGT	1332
Db	1036	GGCCCTTCAGATTTCTTTAAGGCACTTATGATATGCTGCTGTACACTCTTCTTGTGCT	1095
Qy	1333	CTTTGCAATTCCTTTGGCCACAGTGAAGAGAGAGGAGAAATAATATCCAGGCTTAAG	1392
Db	1096	CTCTGCATCTTTTGTGGCTACAAAGGATTCGTGAGCAAGAGAGAGAGCCCTGAGTTTAA	1155
Qy	1393	AGAGCTCTTCAAGTGCATAGAGGGCCAGAAACCGTATATATCTATCTATGTCAGAGAA	1452
Db	1156	AGAGAGCCCTGCAAAATGCAACAGAGGCTCAGAGACAGTTTATCATTTGTATGTTAGAGAA	1215
Qy	1453	AGGGAGGTTTGTAGATGGAGTCCATTTTACCTGAGGCTAGCAATTTAACTCTGAATGCT	1512
Db	1216	AGAGAGCGTTTGTACATGGAATCCATCTTCTTGAAGGATGGAATCTGACTCTGGAAGCT	1275
Qy	1513	GTGAAGGCTGCTGTTGTTTGAAGTTTCAATCCCTCGAATCTTGTGCTGTTATGGAAGACT	1572
Db	1276	CTGGAAATCTCGGGTTCTTGGCAAGTTCTATGCTCTGAGATATGAACCAATATGGAAGAG	1335
Qy	1573	GAAGGCTTGAAGTTATAGAGGGGGAGTCTTTTAAACTCTTAAACTCTCAAAATATACCAATT	1632
Db	1336	GAAGAGCCCGAGCTTAAGAGGAGACGGCAAGCTTAGAGTACATGAGGATATATCTTAT	1395
Qy	1633	GGCTTGACACAGAGACAGCTTTTATACCTTTCAGCTTCAAGGTTGAGTGTGATTTCAAGG	1692
Db	1396	GGTCTGACTCAAGACAGAGCTCTTTTACACTTCAATTTCAATTTCAAGGAAATTCAGTCTCAGT	1455
Qy	1693	AGTCACTTGGAGAAACAATCTTGTGCCAAGTTTGAAGTCAATTTTGTGTA	1742

Db	1456	ACTCACAATACAGAGAAACCTTGTCTCCCAAAATTCGAAGTTGTTCTTGTCTTA	1505	Db	468	GTGATTGTGTAATGGGATTCACCTTCAGATAAGAAACCTGATGCGGCTTTTGGATAAGT	527
RESULT 8	ATH345084	1729 bp	mRNA	linear	PLN 03-OCT-2002		
LOCUS	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana		
DEFINITION	(fucT1 gene).						
ACCESSION	AJ345084						
VERSION	GI:15722479						
KEYWORDS	core-alpha1,3-fucosyltransferase 1; fucT1 gene.						
SOURCE	Arabidopsis thaliana						
ORGANISM	Arabidopsis thaliana						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eutrosids II; Brassicales; Brassicaceae; Arabidopsis.						
AUTHORS	Bakker, H., Schijlen, E., de Vries, T., Schiphorst, W. E., Jordi, W., Lommen, A., Bosch, D. and van Die, I.						
TITLE	Plant members of the alpha1-->3/4-fucosyltransferase gene family encode an alpha1-->4-fucosyltransferase, potentially involved in Lewis(a) biosynthesis, and two core alpha1-->3-fucosyltransferases						
JOURNAL	FEBS Lett. 507 (3), 307-312 (2001)						
PUBLISHED	1169361						
REFERENCE	2 (bases 1 to 1729)						
AUTHORS	Bakker, H.						
TITLE	Direct Submission						
JOURNAL	Submitted (14-SEP-2001) Bakker H., Plant Research International, Wageningen University and Research centre, droevendaalsesteeg 1, Netherlands 6708PB, NETHERLANDS						
FEATURES	Location/Qualifiers						
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ORIGIN							
Query Match	31.4%;	Score 690;	DB 15;	Length 1729;			
Best Local Similarity	72.0%;	Pred. No. 1.8e-157;					
Matches	900;	Conservative	0;	Mismatches 350;	Indels	0;	Gaps
Qy	493	TCTGAATCGTATAGTGTGAGGATGTTGGAGGGAGGAGTCTGTCAGTATTCGAGG	552				
Db	348	TCAGGAATAGAGAAATCCAGAGTGTGTAGAGAGTGGATTTCAGTTACTTATTCAGA	407				
Qy	553	GGCTTTTCCAAAGACCTATTTTGTCTGGAGCTGATCAGGAGTGGAAAGTCGTGTTCG	612				
Db	408	GATTTCATAAGATCCGATTTTATCTCTGGTAGTAACAAGGACTTCAAAATCGTCTCT	467				
Qy	613	GTTGGATGTAATTTGGGTTTAGTGGGGATAGAAAGCCAGATCCCGCATTTGGTTACCT	672				

RESULT 10	
AV117132	
LOCUS	1319 bp mRNA linear PLN 06-MAY-2005
DEFINITION	Arabidopsis thaliana core alpha 1,3-fucosyltransferase mRNA, partial cds.
ACCESSION	AV117132
VERSION	AV117132.1 GI:37545058
KEYWORDS	.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 1319)

AUTHORS Kiefer-Meyer, M.-C., Faye, L. and Gomord, V.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUN-2002) CNRS UMR 6037, Universite de Rouen, Mont Saint Aignan 76821, France
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 QY 733 AACATAATGCCATGCCAAGACGGAGGGATATAACATCGTAATGACCAACAGCTCTATCT 792
 DB 242 AATAATCTGCTCAAGCACGACGGAAGGTTATGATATGTTGATGACACTAGTCTGTCA 301
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 LOCUS Arabidopsis thaliana mRNA for core-alpha1,3-fucosyltransferase 2
 DEFINITION (fucT2 gene).
 ACCESSION AJ345085
 VERSION AJ345085.1 GI:15722481
 KEYWORDS core-alpha1,3-fucosyltransferase 2; fucT2 gene.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
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 Bakker,H., Schijlen,B., de Vries,T., Schiphorst,W.E., Jordi,W.,
 Lommen,A., Bosch,D. and van Die,I.
 Plant members of the alpha1-->3/4-fucosyltransferase gene family
 encode an alpha1-->4-fucosyltransferase, potentially involved in
 Lewis(a) biosynthesis, and two core alpha1-->3-fucosyltransferases
 FEBS Lett. 507 (3), 307-312 (2001)
 JOURNAL PUBMED 11696361
 REFERENCE 2 (bases 1 to 1542)
 AUTHORS Bakker,H.
 TITLE Direct Submission
 JOURNAL Submitted (14-SEP-2001) Bakker H., Plant Research international,
 Wageningen University and Research centr, droevendaalsesteeg 1,
 Netherlands 6708PB, NETHERLANDS
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ORIGIN

Query Match	30.9%;	Score 678.8;	DB 15;	Length 1542;
Best Local Similarity	68.4%;	Pred. No. 9.9e-155;		
Matches 989;	Conservative 0;	Mismatches 442;	Indels 15;	Gaps 3;
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Db	169	GGGTTTCTGGTCGGCTCGAT-----AAAGTCGCTTTGGTTGATACGTTGACTGAT	219	
Qy	421	TTCTTCTACCGCTCTCGAGCGGTGTTGAAGTGACGATTTTGGGTTGGGTTTGGTGGCT	480	
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Qy	661	TTTGGGTTACTCAACCAAGTGGGAACAGCTAGCATTTCTGCGATCAATGGAAATCAGCAGAA	720	
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Db	577	ACTAGTCTATCATCAGATGTTTCTGTGGATATTTTTTTCGTGGCGGAGTATGATATTATG	636	
Qy	841	GCACAGTGCAGCCGAAACCTGAAGCTGCTCTTCAGCTGCTTTTCATTTCCAATTTGTCGT	900	
Db	637	TCTCCGGTACAGCAAAACCTGAGAGAGCTATTCAGCTGCTTTTATTTTCTTAATTTGTCGT	696	
Qy	901	GCTCGAAATTTCCGGTTGCAAGCTCTTCGAGGCCCTTTGAAAATTAACAAATTCAAATTTGAT	960	

[illegible]

RESULT 12	AY184990	1607 bp	mrna	linear	PLN 02-MAR-2005
LOCUS	AY184990				
DEFINITION	Arabidopsis thaliana core alpha 1, 3-fucosyltransferase mRNA, complete cds.				
ACCESSION	AY184990				
VERSION	AY184990.1 GI:37731907				
KEYWORDS	.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				

REFERENCE	1 (bases 1 to 1607)
AUTHORS	Kiefer-Meyer,M.-C., Faye,L. and Gomord,V.
TITLE	Direct Submission
JOURNAL	Submitted (21-NOV-2002) CNRS UMR 6037, Universite de Rouen, Batiment Extension Biologie, Mont Saint Aignan 76821, France
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ORIGIN	
Query Match	30.9%; Score 678.8; DB 15; Length 1607;
Best Local Similarity	68.4%; Pred. No. 9.8e-155;
Matches	989; Conservative 0; Mismatches 442; Indels 15; Gaps 3;
QY	301 AAGAGGAAATGGACCAATCTAATGCCTCTTTGTTGTTGCCCTTGTGTGTCATGCGGAGATC 360
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RESULT 13	
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LOCUS	Arabidopsis thaliana Putative fucosyltransferase (At1g49710) mRNA,
DEFINITION	complete cds.
ACCESSION	BT002570
VERSION	BT002570.1 GI:27311928
KEYWORDS	FLI CDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS

1. (bases 1 to 1725)
 Nguyen,M., Southwick,A., Tripp,M., Palm,C.J., Jones,T., Wu,T.,
 Carninci,P., Chen,H., Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M.,
 Deng,J.M., Hayashizaki,Y., Hsuan,V.W., Lee,J.M., Ishida,J.,
 Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Onodera,C.S.,
 Quach,H.L., Sakurai,T., Satou,M., Seki,M., Shim,P., Tang,C.C.,
 Toroumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S.,
 Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
 Direct Submission
 Submitted (20-DEC-2002) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 e-mail for correspondence: arab@sequence.stanford.edu

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
 Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Sh inozaki,K.

The Salk, Stanford, PGBC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Nguyen,M., Tripp,M.,
 Southwick,A., Palm,C.J., Jones,T., Wu,T., Chen,H., Cheuk,R.,
 Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M.,
 Kim,C.J., Quach,H.L., Onodera,C.S., Shinn,P., Tang,C.C.,
 Toroumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Ecker,J.,
 Theologis,A. and Davis,R.W.

Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
 equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
 (SSP/Stanford) contributed equally to this work as PIs.

FEATURES
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 EVFVY"

ORIGIN

Query Match 30.9%; Score 678.8; DB 15; Length 1725;
 Best Local Similarity 68.4%; Pred. No. 9.8e-155;
 Matches 999; Conservative 0; Mismatches 442; Indels 15; Gaps 3;
 301 AAGAGAAATGAGCAATCAATGCTCTTGTGTTGCCCTTGTGCTATCCGAGATC 360
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REFERENCE					
AUTHORS	Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,				
	Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,				
	Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,				
	Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,				
	Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,				
	Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.				
	Direct Submission				
TITLE	Submitted (28-AUG-2001) DNA Sequencing and Technology Center,				
JOURNAL	Stanford University, 855 California Avenue, Palo Alto, CA 94304,				
	USA				
COMMENT	e-mail for correspondence: arab@sequence.stanford.edu				
	RIKEN Genomic Sciences Center (GSC) members carried out the				
	collection and clustering of RAFL cDNAs (RAFL cDNA : "RIKEN				
	Arabidopsis Full-Length cDNA") : Seki,M., Narusaka,M., Ishida,J.,				
	Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Carninci,P., Kawai,J.,				
	Hayashizaki,Y. and Shinozaki,K.				
	The Salk, Stanford, PDEC (SSP) Consortium members carried out the				
	sequencing and annotation of the RAFL cDNAs: Nguyen,M.,				
	Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,				
	Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,				
	Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,				
	Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.				
	Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed				
	equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.				
	(SSP/Stanford) contributed equally to this work as PIs.				
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 VERSION AV184991.1 GI:37731911
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 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
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 Kiefer-Meyer M.-C., Faye, L. and Gomord, V.
 Direct Submission
 Submitted (21-NOV-2002) CNRS UMR 6037, Universite de Rouen, Batiment Extension Biologie, Mont Saint Aignan 76821, France
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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AC AAA97937;
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XX 15-SEP-2003 (revised)
DT 26-JAN-2001 (first entry)
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KW GlnAC-alpha1,3-fucosyl transferase; ds.
KW
XX Vigna radiata var. radiata.
OS
XX WO200049153-A1.
FN
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PD
XX 17-FEB-2000; 2000WO-AT000040.
PF
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PA
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FI
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XX
XX DNA encoding plant GlnAC-alpha-1,3-fucosyl transferase, useful for
PT recombinant production of the enzyme and recombinant glycoprotein
PT production.
PS Claim 1; Page 35-36; 72pp; German.
XX
CC This invention describes a novel DNA molecule (I), encoding a plant
CC protein with fucosyl transferase activity, GlnAC-alpha1,3-fucosyl
CC transferase. The methods and DNA sequences are useful for production of
CC recombinant GlnAC-alpha1,3-fucosyltransferase. The enzyme is useful for
CC the production of recombinant human glycoproteins, which are especially

CC useful in medical applications and pharmaceutical compositions. (I) can
be used as a probe to select GlcNAc-alpha1,3-fucosyltransferase coding
CC sequences in a sample, especially from plants or insects. This sequence
CC encodes the mung bean (Phaseolus aureus) alpha 1,3-fucosyltransferase
CC protein described in the method of the invention. (Updated on 15-SEP-2003
CC to standardise OS field)
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QY 1021 CACTACAAATTTAGCTTTAGCGTTTGAANAATTCGAATGAGGAAGATTTATGTAACGTAAAAA 1080
DB 1021 CACTACAAATTTAGCTTTAGCGTTTGAANAATTCGAATGAGGAAGATTTATGTAACGTAAAAA 1080

QY 1081 TCTTCCAAATCCCTTGTGTGCGAACTGTCCCTGTGGTTGTGTGCTGCCAAATATTCAG 1140
DB 1081 TCTTCCAAATCCCTTGTGTGCGAACTGTCCCTGTGGTTGTGTGCTGCCAAATATTCAG 1140

QY 1141 GACTTTGCTCCTCTCTCTGGTTCAATTTTACATATTTAAAGAGATAGAGGATGTTGAGTCT 1200
DB 1141 GACTTTGCTCCTCTCTCTGGTTCAATTTTACATATTTAAAGAGATAGAGGATGTTGAGTCT 1200

QY 1201 GTTGCAAGAACAATGAGATATCTAGCAAAAATCCCGAAGCATATAATCAATCATTTGAGG 1260
DB 1201 GTTGCAAGAACAATGAGATATCTAGCAAAAATCCCGAAGCATATAATCAATCATTTGAGG 1260

QY 1261 TGGAGTATGAGGGTCCATCTGACCTTTCAAGGCCCTTTGGATATGCGAGCTGTGCAT 1320
DB 1261 TGGAGTATGAGGGTCCATCTGACCTTTCAAGGCCCTTTGGATATGCGAGCTGTGCAT 1320

QY 1321 TCATCGTCCCGTCTTTTGTGCAATTCATTTGGCCACAGTGAGTAGAGGAAGAAATAAT 1380
DB 1321 TCATCGTCCCGTCTTTTGTGCAATTCATTTGGCCACAGTGAGTAGAGGAAGAAATAAT 1380

QY 1381 CCAAGCCTTAAGAGACGCTCTTGAAGTGCATAGAGGCCCAAGAACCGTATATCATATC 1440
DB 1381 CCAAGCCTTAAGAGACGCTCTTGAAGTGCATAGAGGCCCAAGAACCGTATATCATATC 1440

QY 1441 TATGTACAGAAAGGGGAGGTTTGAGATGGATGCCATTTACCTCAGGCTCTAGCAATTTA 1500
DB 1441 TATGTACAGAAAGGGGAGGTTTGAGATGGATGCCATTTACCTCAGGCTCTAGCAATTTA 1500

QY 1501 ACTCTGAATGCTGTGAAGGCTGCTGTTGTTTGAAGTTTCAATCCCTGAATCTTGTGCT 1560
DB 1501 ACTCTGAATGCTGTGAAGGCTGCTGTTGTTTGAAGTTTCAATCCCTGAATCTTGTGCT 1560

QY 1561 GTATGGAAGACTGAAAGGCTGAAAGTGTATAGAGGGGGAGTGTCTTAAACCTCTACAA 1620
DB 1561 GTATGGAAGACTGAAAGGCTGAAAGTGTATAGAGGGGGAGTGTCTTAAACCTCTACAA 1620

QY 1621 ATATACCCAAATTTGGCTTGACACAGAGCAAGCTCTTTATACCTTCAGCTTTCAAAGGTGAT 1680
DB 1621 ATATACCCAAATTTGGCTTGACACAGAGCAAGCTCTTTATACCTTCAGCTTTCAAAGGTGAT 1680

QY 1681 GCTGATTTTCAAGAGTCACTTTGGAGAAACATCTCTGTGCCAAGTTTGAAGTCAATTTTGTG 1740
DB 1681 GCTGATTTTCAAGAGTCACTTTGGAGAAACATCTCTGTGCCAAGTTTGAAGTCAATTTTGTG 1740

QY 1741 TAGCATGCGCTAAATGGTACCTCTGCTCTACCTGAAATAGCTCTTATACCTTCAGCTTTCAAAGGTGAT 1800
DB 1741 TAGCATGCGCTAAATGGTACCTCTGCTCTACCTGAAATAGCTCTTATACCTTCAGCTTTCAAAGGTGAT 1800

QY 1801 GCTAGAGTTTATAGGAATGAGTATGGCAATATGCGCATGGCTTTATTTATGCGCTAGTT 1860
DB 1801 GCTAGAGTTTATAGGAATGAGTATGGCAATATGCGCATGGCTTTATTTATGCGCTAGTT 1860

QY 1861 TCTTGGCCAACTCAATTTATGATGTTTGTATAGGATCATCACTTTAAATTTAAACTTGTTC 1920
DB 1861 TCTTGGCCAACTCAATTTATGATGTTTGTATAGGATCATCACTTTAAATTTAAACTTGTTC 1920

QY 1921 TGTAGAAGTGCAAATCCATTTATGCTTTAGTGTCTTTAGTGTCTTTATCTGATCATCTAGA 1980
DB 1921 TGTAGAAGTGCAAATCCATTTATGCTTTAGTGTCTTTAGTGTCTTTATCTGATCATCTAGA 1980

QY 1981 AGTCACAGTTCTTGATATTTGTGAGTGAATACTGAAATCTAATAGAAGGATCAGATGTTT 2040

Db 1981 AGTCACAGTCTTGTATATTGTGAGTGAACCTGAAATCTAATAGAGGATCAGATGTTT 2040
QY 2041 CACTCAAGACACATTATTACTTCATGTTGTTTGTGATGATCTCAGCTTTTATTAGTCTG 2100
Db 2041 CACTCAAGACACATTATTACTTCATGTTGTTTGTGATGATCTCAGCTTTTATTAGTCTG 2100
QY 2101 GAATGTCCTCTGTTGTTGAGCACCTGTTATTGCTTCAGTGTACTGTCAGTGGTTATC 2160
Db 2101 GAATGTCCTCTGTTGTTGAGCACCTGTTATTGCTTCAGTGTACTGTCAGTGGTTATC 2160
QY 2161 GTTTTTCACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 2198
Db 2161 GTTTTTCACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 2198

RESULT 2

ADT15744
ID ADT15744 standard; cDNA; 2036 BP.

XX ADT15744;

DT 13-JAN-2005 (first entry)

DE Plant cDNA, Seq ID 1070.

XX Plant; ss; gene; transgenic; cold tolerance; growth rate;

KW drought tolerance; disease resistance; galactomannan production;

KW plant growth regulator; heat tolerance; herbicide tolerance;

KW lignin production; extreme osmotic condition tolerance;

KW pathogens resistance; pest resistance; yield improvement; seed oil yield;

KW seed protein yield.

XX Viridiplantae.

XX US2004216190-A1.

XX 28-OCT-2004.

XX 18-DEC-2003; 2003US-00739930.

XX 28-APR-2003; 2003US-00424599.

PR 28-APR-2003; 2003US-00425115.

XX (KOVA/) KOVALIC D K.

XX KOvalic DK;

XX WPI; 2004-757369/74.

XX New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.

PS Claim 1; SEQ ID NO 1070; 14pp; English.

CC The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving

CC plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant cDNA sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX Sequence 2036 BP; 596 A; 392 C; 446 G; 602 T; 0 U; 0 Other;

QY Query Match 30.2%; Score 664.8; DB 13; Length 2036;

Db Best Local Similarity 68.2%; Pred. No. 1.1e-166;

XX Matches 989; Conservative 0; Mismatches 442; Indels 19; Gaps 4;

QY 301 AAGAGAAATGGAGCAATCTAATGCTCTTGTGTTGCTCTGTCATCGGGAGATC 360

Db 268 AAGCGAAATATTCGAAATTTGTTACCACCTCTCGGTGTCTGTTAGTATTCGCTAGATC 327

QY 361 GCGTTTCTGGTAGGTTGGATATGGCCAAAACGCGCCATGTTGACTCCCTCGCTGAC 420

Db 328 GGGTTTCTGGTCTGGCTCGAT-----AAAGTCGTTTGGTTGACTGAT 378

QY 421 TTCTTCTACCGTCTCGAGCGGTGTTGAAGTGAAGTATTTGGGGTTGGGTTTGGTGGCT 480

Db 379 TTCTTCAACCCAGTCTCCGTCCTCTCCAGTCTCCACCGCGAGATCCGATCGGAAGAAG 438

QY 481 TCTGATCGGAATTCCTGAATCGTATAGTCTGAGGAATGTTGGAGAGGAGGATGCTGTC 540

Db 439 ATCGGAATATTTACTGATAGG---AGCTCGAGGAGTGGTTGATGAGAAAGTATTCAGTT 495

QY 541 ACGTATTCGAGGGGCTTTTCCAAAGAGCCTATTTTGTCTCGAGCTGATCAGGAGTGG 600

Db 496 ACTTACTTAGAGATTTTACTAAAGATCCAAATTTTATCTCTGCTGCTGAAGGACTTT 555

QY 601 AAGTCGTGTTGCGTTCGATGTAAATTTGGGTTTAGTGGGGATAGAAAGCCAGATCGCGCA 660

Db 556 CAATGGTGTCTGTGGATTGTACATTTGGAGATAGTTTCAGGGGAAAACACAGATGCTGCG 615

QY 661 TTTGGGTTTACCTCAACCAAGTGAACAGCTAGCAATTCGCGATCAATGGAATCAGCAGAA 720

Db 616 TTTGGATTAGGTCAGAAACCTGGAACTCTTAGTATTAATAGTTCATGGGAATCAGACAG 675

QY 721 TACTATGCTGAGAAACAATATTGCGATGCGAAGACGGAGG---GGATATAACATCGTAAT 776

Db 676 TATTATCCAGAAATATGATCTTGACAGGCACGACGCTGGAGAGGTTATGATATAGTAT 735

QY 777 GACAAACAGTCTATCTTCGGATGTTCTCTGTTGGATATTTTTCATGGGCTGAGTATGATAT 836

Db 736 GACCACCTAGTCTATCATCAGATGTTCTCTGTTGGATATTTTTCGTTGGCGGAGTATGATAT 795

QY 837 GATGGACCAAGTCACCGCAAAACTGAGCTCTTGGAGCTGCTTTCATTTCCCAATTG 896

Db 796 TATGTCCTCGGTACACCAACCACTGAGAGAGCTATTCGAGCTGCTTTTATTTCTAATTG 855

QY 897 TGTGTCGAAATTTTCCGGTTTGAAGCTCTTGGAGGCTTTGAAAATCAAAATCAAAAT 956

Db 856 TGTGTCGGAATTTTTCGTTCTACAGCACTTGAGGCAATGATGAAACTTAACATTAGAT 915

QY 957 TGAATTCCTTAGTGGTGTGTCACAGGAACCGTGTAGTGAAGAGTGAAACAAAGTGAAGCCCT 1016

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Db	916	TGATTCCTTATGGTGGTTGTCATCGAAACCGGATGGGAAAGTTGACAAAGTTGAAGCTCT	975	PD	06-SEP-2000.
Qy	1017	GAAGCACTACAAATTTAGCTTAGCGTTTGAAAATTCGAATCAGGAAGATTATGTAACCTGA	1076	XX	25-FEB-2000; 2000EP-00301439.
Db	976	TAGCGATACAAATTCAGTTTGGCTTTTGAGATACTAACGAGGAAGATTATGTCACCGA	1035	XX	25-FEB-1999; 99US-0121825P.
Qy	1077	AAAAATCTTCCAAATCCCTTGTGTGGAACTGTCCCTGTGGTTGTGTGCTCCAAATAT	1136	PR	05-MAR-1999; 99US-0123180P.
Db	1036	GAGTTCCTTCAATCCTTAGTTGCTGGTCCGTCCTCCCTGGTAGTTGGTCTCCCAATAT	1095	PR	09-MAR-1999; 99US-0125788P.
Qy	1137	TCAGGACTTGTCTCTCTCGGTTCAAATTTTACATATTAAGAGATAGAGAGTTGA	1196	PR	23-MAR-1999; 99US-0126264P.
Db	1096	AGAAGAAATTCGGCTCTCTCGGACTCAATTCCTTCAATTAAGACTATGGAAGATGTGA	1155	PR	25-MAR-1999; 99US-0126785P.
Qy	1197	GTCTGTGCAAGACCACTGAGATATCTAGCAGAAAATCCGAAAGCATATAATCAATCAT	1256	PR	01-APR-1999; 99US-0127462P.
Db	1156	GCCAGTTGCAAGAGAAATGAAGTATCTGCAGCTAACCTGCTGCTTATTAATCAGACACT	1215	PR	06-APR-1999; 99US-0128234P.
Qy	1257	GAGGTGGAAGTATGAGGTCCTATCTGACTCCTTCAAGGCCCTTGTGGATATGGCAGCTGT	1316	PR	08-APR-1999; 99US-0128714P.
Db	1216	AGATGGAATACGAGGGTCTTTCAGATCTTTTCAAGGCACCTTGTATGATGCTGCTGT	1275	PR	16-APR-1999; 99US-0129845P.
Qy	1317	GCATTCATCGTCCGCTCTTTCGATTCACCTTGGCCACAGTGTAGTAGAGAGAGAGAAA	1376	PR	19-APR-1999; 99US-0130077P.
Db	1276	ACACTCTTCTTCCGCTCTCTGCATTTTCTGCGCACGAGGGTCCGAGAAACAAGAGAGGA	1335	PR	21-APR-1999; 99US-0130449P.
Qy	1377	TAATCCAAGCCTTAAGAGACGCTCTTTCGAAGT---GCACCTAGAGGGCCAGAAACCGTATA	1433	PR	23-APR-1999; 99US-0130510P.
Db	1336	AGCCCTTAATTTCAAGAAACGACCGTGCAATGTAGCAGGGAGGATCAGACACATTTA	1395	PR	28-APR-1999; 99US-0130891P.
Qy	1434	TCATATCTATGTCCAGAGAAAGGGAAAGGTTTGAGATGGAGTCCATTTACTGAGGTCATG	1493	PR	30-APR-1999; 99US-0131449P.
Db	1396	TCATGTTTTTTTAGAGAAAGAGCGCGTTTGAATGGAATCAGTCTTTTTCAGGGGGTAA	1455	PR	30-APR-1999; 99US-0132048P.
Qy	1494	CAATTTAATCTGAATGCTGTGAAGCTGCTGTTGTTTGAAGTTTCAATCCCTGAATCT	1553	PR	04-MAY-1999; 99US-0132484P.
Db	1456	AAGTGTGACTCAGGAAGCTCTAGAACTCTGCAGTTCTCGCCAAAGTTCAGTCTTTAAACA	1515	PR	05-MAY-1999; 99US-0132485P.
Qy	1554	TGTGCTGTATGAAGCACTGAAGGCTGAAGTTTATAAGAGGGGGAGTGTCTTTAAAACT	1613	PR	06-MAY-1999; 99US-0132486P.
Db	1516	TGAGGCAGTGTGGAAGAAAGAAAGGCTTGAACTTAAAGGAGACAAAGAGCTTAAAT	1575	PR	07-MAY-1999; 99US-0132863P.
Qy	1614	CTACAAATATACCCCAATTCGCTTGACACAGAGACAAAGCTCTTTATACCTTCAGCTTCAA	1673	PR	11-MAY-1999; 99US-0134256P.
Db	1576	ACATCGGATTTACCCGCTTGCCCTTAACGCAACGACAGGCTTTGTACAACTTCAAATTCGA	1635	PR	14-MAY-1999; 99US-0134218P.
Qy	1674	AGGTGATGCTGATTTTCAGGAGTCACTTGGAGAACAAATCCTTGTGCCAAGTTTGAAGTCAT	1733	PR	14-MAY-1999; 99US-0134219P.
Db	1636	GGGAAATTCGAGTCTAAGTAGTACATTCAAATTCAAACCAACCCCTTGTCTAAATTTGAGGTGT	1695	PR	14-MAY-1999; 99US-0134370P.
Qy	1734	TTTTGTGTAG 1743		PR	18-MAY-1999; 99US-0134768P.
Db	1696	CTTCGTCTAG 1705		PR	18-MAY-1999; 99US-0134941P.
RESULT 3					PR 19-MAY-1999; 99US-0135124P.
AAC39529					PR 20-MAY-1999; 99US-0135353P.
XX	AAC39529 standard; DNA; 1982 BP.				PR 21-MAY-1999; 99US-0135629P.
AC	AAC39529;				PR 24-MAY-1999; 99US-0136021P.
XX	17-OCT-2000 (first entry)				PR 25-MAY-1999; 99US-0136392P.
DT	Arabidopsis thaliana DNA fragment SEQ ID NO: 24967.				PR 27-MAY-1999; 99US-0136782P.
XX	Hybridisation assay; genetic mapping; gene expression control;				PR 28-MAY-1999; 99US-0137222P.
XX	protein identification; signal transduction pathway; metabolic pathway;				PR 03-JUN-1999; 99US-0137528P.
KW	promoter; termination sequence; ss.				PR 04-JUN-1999; 99US-0137502P.
XX	Arabidopsis thaliana.				PR 07-JUN-1999; 99US-0137724P.
OS	EP1033405-A2.				PR 08-JUN-1999; 99US-0138094P.
XX					PR 10-JUN-1999; 99US-0138540P.
PN					PR 10-JUN-1999; 99US-0138847P.
					PR 14-JUN-1999; 99US-0139119P.
					PR 16-JUN-1999; 99US-0139452P.
					PR 16-JUN-1999; 99US-0139453P.
					PR 17-JUN-1999; 99US-0139492P.
					PR 18-JUN-1999; 99US-0139454P.
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					PR 18-JUN-1999; 99US-0139750P.
					PR 18-JUN-1999; 99US-0139763P.
					PR 18-JUN-1999; 99US-0139817P.
					PR 21-JUN-1999; 99US-0139899P.
					PR 22-JUN-1999; 99US-0140353P.
					PR 23-JUN-1999; 99US-0140354P.
					PR 23-JUN-1999; 99US-0140695P.
					PR 24-JUN-1999; 99US-0140823P.
					PR 28-JUN-1999; 99US-0140991P.
					PR 29-JUN-1999; 99US-0141287P.
					PR 30-JUN-1999; 99US-0141842P.
					PR 01-JUL-1999; 99US-0142154P.
					PR 01-JUL-1999; 99US-0142055P.
					PR 02-JUL-1999; 99US-0142055P.

PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-01435542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144684P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161922P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161933P.
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161934P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147192P.			
PR	05-AUG-1999;	99US-0147260P.			
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.			
PR	09-AUG-1999;	99US-0147493P.			
PR	09-AUG-1999;	99US-0147935P.			
PR	10-AUG-1999;	99US-0148171P.			
PR	11-AUG-1999;	99US-0148319P.			
PR	12-AUG-1999;	99US-0148341P.			
PR	13-AUG-1999;	99US-0148565P.			
PR	13-AUG-1999;	99US-0148684P.			
PR	16-AUG-1999;	99US-0149368P.			
PR	17-AUG-1999;	99US-0149175P.			
PR	18-AUG-1999;	99US-0149426P.			
PR	20-AUG-1999;	99US-0149722P.			
PR	20-AUG-1999;	99US-0149723P.			
PR	20-AUG-1999;	99US-0149923P.			
PR	23-AUG-1999;	99US-0149902P.			
PR	23-AUG-1999;	99US-0149930P.			
PR	25-AUG-1999;	99US-0150566P.			
PR	26-AUG-1999;	99US-0150884P.			
PR	27-AUG-1999;	99US-0151065P.			
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PR	27-AUG-1999;	99US-0151080P.			
PR	30-AUG-1999;	99US-0151303P.			
PR	31-AUG-1999;	99US-0151438P.			
PR	01-SEP-1999;	99US-0151930P.			
PR	07-SEP-1999;	99US-0152363P.			
PR	10-SEP-1999;	99US-0153070P.			
PR	13-SEP-1999;	99US-0153758P.			
PR	15-SEP-1999;	99US-0154018P.			
PR	16-SEP-1999;	99US-0154039P.			
PR	20-SEP-1999;	99US-0154779P.			
PR	22-SEP-1999;	99US-0155139P.			

Query Match		30.1%;	Score 661.6;	DB 3;	Length 1982;
Best Local Similarity		68.1%;	Pred. No. 7.9e-166;		
Matches 987;		Conservative	0;	Mismatches 444;	Indels 19; Gaps 4;
Qy	301	AAGAGGAAATGGAGCAATCTAATGCCCTCTTGTGTTGCTCCCTTGTGGTCATCGCGAGATC	360		
Db	267	AAGGAAATATCGAATTTGTTACCACTCTGGTGTCTCTGGTAGTTATCGCTGAGATC	326		
Qy	361	GCCTTTCTGGGTAGTTGGATATGGCCAAACGCCGCCCATGGTTGACTCCCTGGCTGAC	420		
Db	327	GGGTTTCTGGTGGCTCGAT-----AAAGTCGTTTGGTTGATACGTTGACTGAT	377		
Qy	421	TTCTTTACCGCTCTCGAGCGGTGTTGAAGGTGACGATTTGGGTTGGGTTGGTGGCT	480		
Db	378	TTCTTACCAGTCTCGTCACTCTCGCAGTCTCCACGGCGAGATCCGATCGGAAGAAG	437		
Qy	481	TCTGATCGGAATTTCTGAATCGTATAGTTGTGAGGAATGGTTGGAGGGAGGATGCTGTC	540		
Db	438	ATCGGATTTATTACTGATAGG---AGCTCGAGAGGTGGTTGATGAGAAGATTCAGTT	494		
Qy	541	ACGTATTTCGAGGGGCTTTTCCAAAGAGCCCTATTTTCTTCTGGAGCTGATCAGGAGTGG	600		
Db	495	ACTTACTCTAGAGATTTTACTTAAGATCCAAATTTTATCTCTTGTGTGTAAGGACTTT	554		
Qy	601	AAGTCGTTTCGGTTGGATGTAATTTGGGTTTAGTGGGATGAAGACGAGATGCCGCA	660		
Db	555	CAATGGTGTCTGTGGATTGTACATTTGGAGATAGTTTCAGGGAAAAACACAGATGCTGCG	614		
Qy	661	TTTGGGTACTCTCAACCAAGTGGACAGCTAGCATTTCTGCATCAATGGATCAGCAGAA	720		
Db	615	TTTGGATTAGTCAGAAACCTGGAACTCTTTAGTATATAATACGTTCCATGGATCAGCAG	674		
Qy	721	TACTATGCTCAGAACAAATATTGGCATTCGCAAGACGGAGG---GGATATTAACATCGTAAT	776		

Db	675	TATTATCCAAAAATGATCTTTGCACAGGCACGCGTGGGAGAGGTTATGATATAGTGAT	734
Qy	777	GACAAACAGTCTATCTTCGGATGTTCTCTGTTTGGATATTTTTTCATGGGCTGAGTATGATAT	836
Db	735	GACCACTAGTCTATCATCAGATGTTCTCTGTTGGATATTTTTCTGTTGGCGGAGTATGATAT	794
Qy	837	GATGGCACCAAGTGCAGCGGAAAACATGAAGCTCTCTTCGACGCTGCTTTTCATTTCCAAATTG	896
Db	795	TATGTCTCCGGTACAGCCAAAACCTGAGAGAGCTATTCGACGCTGCTTTTATTTCTTAATTG	854
Qy	897	TGTTGCTCGAAAATTTCCGGTTGCAAGCTCTTGAGGCGCTTGAAAAATCAAAACATCAAAAT	956
Db	855	TGTTGCTCGAAAATTTTCGTTCTACAAGCACTTGAGGCAATTCATGAAAACTAAACATTAAGAT	914
Qy	957	TGATTTCTTATGTTGGTTGTCACAGGAACCGTGTATGGAAGAGCTGAACAAAGTGGAGCCCT	1016
Db	915	TGATTTCTTATGTTGGTTGTTCATCGAAAACCGGATGGAAAAGTTGAACAAGTTGGAAGCTCT	974
Qy	1017	GAAGCACTACAAATTTAGCTTTAGCGTTTGAATAATTCGAATGAGGAAGATTATGTAACTGA	1076
Db	975	TAAAGCATACAAATTTCAAGTTTGGCTTTTGAGAAATCTAACAGGAGAATATATGTCACCGA	1034
Qy	1077	AAAATTTCTTCCAAATCCCTTGTGCTGGAACTGCTCCCTGTGGTTGTTGGTCTCCAAATAT	1136
Db	1035	GAAGTTCTTTCAATCCCTTAGTTGCTGGTCCGTCCTGGTGGTAGTTGGTCTTCCCAATAT	1094
Qy	1137	TCAGGACTTTGCTCCTTCTCTCTGTTTCAATTTTACATATTAAGAGATAGAGATCTTGA	1196
Db	1095	AGAAGATTTGCGCTGCTTTCGGACTCATTTCTTTCATTTAAGCACTATGGAAGATGTAGA	1154
Qy	1197	GTCTGTTGCAAGACCATTGAGATATCTAGCAGAAAAATCCGGAAGCATATAATCAATCAAT	1256
Db	1155	GCCAGTTGCAAGAAGAAATGAAGTATCTCGCAGTACCCCTGCTCTTATTAATCAGACACT	1214
Qy	1257	GAGGTGAAGATATGAGGCTCCATCTGACTCTCTTCAAGGCCCTTTGTGGATATGCGACTGT	1316
Db	1215	AAGATGGAATATACGAGGCTCTTTCAGATTTCTTTCAGGSCATTTGTTGATGCTGCTGT	1274
Qy	1317	GCAATTCATCGTCCGCTTTTGCAATTCATTGGCCACAGTGAAGTAGAGAGAAGCAAGAAA	1376
Db	1275	ACACTCTTCTTGCGCTCTCTGCAATTTCTGSCCACGAGGCTCCGGAACAAGAGAGGA	1334
Qy	1377	TAAATCCAAGCCTTAAGAGACGCTCTTTCGCACT--GCACCTAGAGGGCCAGAAACCGTATA	1433
Db	1335	AAGCCCTAATTTCAAGAAGACGACCGTGAAATGTAGACGGGAGGATCAGACAGATTTA	1394
Qy	1434	TCATATCTATGTACAGAAAAGGGAGGTTTGGATGGAGTCCATTTTACCTGAGGCTTAG	1493
Db	1395	TCATGTTTTTGTAGAAAAGAGGCGGTTTTGAAATGGAATCACTCTTTTGTAGGGGTAA	1454
Qy	1494	CAATTTAACTCTGAATGCTGAAGGCTGTGTTGTTTTGAGTTTCATATCCCTGATCT	1553
Db	1455	AAGTGTGACTCAGGAAGCTCTAGAAATCTGCATTTCTGCCAAGTTCAAGTCTTTTAAACA	1514
Qy	1554	TGTGCTCTGTATGGAAGACTGAAAGGCTCTGAAGTTATAAGGGGGAGTGCTTTTAAACT	1613
Db	1515	TGAGGCAGTGTGGAAGAAGAAAGGCTTGGAACCTTTAAAGAGACAAAGAGCTTAAAT	1574
Qy	1614	CTACAAAATATACCCAAATTTGGCTTGACACAGAGACAAGCTCTTTATACCTTCAGCTCAA	1673
Db	1575	ACATCGAATTTACCGCTTTGGCTTAACGCAACGACAGGCTTTGTACAACTTCAAATTCGA	1634
Qy	1674	AGGTGATGCTGATTTTCAGGAGTCACTTGGAGAACAACTCTTGTGCAAGTTTGAAGTCAT	1733
Db	1635	GGGAAATTCGAGTCTAAGTAGTACATTTCAAACAACCCCTGTGTCTAAATTTGAGGTGT	1694
Qy	1734	TTTTGTGTAG	1743
Db	1695	CTTCGCTAG	1704

ID	ADX62531 standard; cDNA; 1790 BP.
XX	
AC	ADX62531;
XX	
XX	21-APR-2005 (first entry)
DT	
XX	plant full length insert polynucleotide seqid 33374.
XX	
XX	plant protectant; plant growth regulant; gene therapy; plant;
KW	recombinant DNA construct; physical array; plant breeding marker;
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;
KW	growth rate; cell cycle pathway; disease resistance;
KW	galactomannan production; lignin production; plant growth regulator;
KW	yield; plant growth; plant development; seed oil; protein yield;
KW	protein content; gene; ss.
XX	
OS	Unidentified.
XX	
XX	US2004034888-A1.
PN	
XX	19-FEB-2004.
PD	
XX	
XX	28-APR-2003; 2003US-00425114.
PF	
XX	
PR	06-MAY-1999; 99US-00304517.
PR	05-NOV-2001; 2001US-00985678.
XX	
PA	(LIU//) LIU J.
PA	(ZHOU//) ZHOU Y.
PA	(KOVA//) KOVALIC D K.
PA	(SCRE//) SCREEN S E.
PA	(TABAS//) TABASKA J E.
PA	(CAOY//) CAO Y.
XX	
PI	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX	
XX	WPI; 2004-180133/17.
DR	
XX	
PT	New recombinant DNA construct, useful for improving plant tolerance to
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT	pests, for conferring increased resistance to plant disease, or for
PT	improving yield.
XX	
PS	Claim 1; SEQ ID NO 33374; 15pp; English.
XX	
CC	The invention describes a recombinant DNA construct comprising a
CC	polynucleotide consisting of a sequence encoding an amino acid sequence
CC	available in electronic form from the US patent office at
CC	ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC	of the invention are also useful in physical arrays of molecules and as
CC	plant breeding markers. The recombinant DNA construct is useful for
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in
CC	plant cells by modification of the cell cycle pathway, for conferring
CC	increased resistance to plant disease, for increasing the rate of homologous
CC	recombination in plants, for improving yield by modification of
CC	lignin or plant growth regulators, for increasing the rate of homologous
CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC	or by providing improved plant growth and development under at least one
CC	stress condition or for modifying seed oil or protein yield and/or
CC	content. This sequence represents a plant full length insert
CC	polynucleotide that can be used in the recombinant DNA construct of the
CC	invention.
CC	

[illegible]

Db 166 AGCGCGCGCTGGGGTGTCTCTCTGCGCTCTCTGTTGGCGCGCTTCCTCGCGGAGATC 225
 QY 361 GCGTTTCTGGGTAGTTGGATATGCGCCAAAGACGCGCCATGTTGACTCCCTCGCTGAC 420
 Db 226 GCGTTCTCGCGCGCTCGACATGCGCAAGAACGCCGAGCGGTGAGAGCTGGACACC 285
 QY 421 TTCTTCTACCGCTCTCGAGCGGTGTTTGAAGGTGACGATTGGGGTGTGGGTGCGCT 480
 Db 286 TCCTTTTACCGCGCTCGCGGATTTGGCGGATCGCGTGGCGGGCGCGAGCTCGAGG 345
 QY 481 TCTGATCGGAATTTCTGATCGTATAGT-----TGTGAGAAATGTTGGAGAGGAG 531
 Db 346 GCAGGCGCGACAGCGAGGACGAGAGATCGCGGTGTCGAGCAGCGCTCGAGAGGGAG 405
 QY 532 GATGCTGTACGATTTCCAGCGGCTTTTCCAAAGAGCCTATTTTGTCTGAGCTGAT 591
 Db 406 GATGCGCGCTTACGACCGGACTTTGACAGTGATCCCGTGTGTCGGTGGCGCTGCC 465
 QY 592 CAGGAGTGAAGTGTGTTCCGTTGGATGTAAATTTGGGTTTGTAGTGGGATAGAAAGCCA 651
 Db 466 AAGGATTGGAATAAATCTACGTAGGATGTGAATTTGGTTTCTCGAGTAAGACACCT 525
 QY 652 GATGCCCGATTTGGGTACCTCAACCAAGTGAACAGCTAGCATTTCTGCGATCAATGGAA 711
 Db 526 GATGCTACATTTGGAATTCACCAAGATCTTCTGTAGATGATTCCTCAGATCAATGGAA 585
 QY 712 TCAGCAGAACTATCTGAGACAAATATTCATGCGCAAGAGCGGGGATATACATC 771
 Db 586 TCATCTCAATATTATTCAGAGATAATATTGATGTGGCTCGAGGAGAGGTTACAAGATT 645
 QY 772 GTAATGACAAACCACTCTATCTTCGGATGTTCTGTTGGATATTTTTCATGGCTGAGTAT 831
 Db 646 GTGATGACAAACCACTCTTCTCAGAGTACCACTTGGCTACTTTTCATGGCTGATAT 705
 QY 832 GATATGATGACACAGTGCAGCGCGAAATGAAAGTCTCTTCAGCTGCTTTTCATTTC 891
 Db 706 GATATCATGCACTGTGCGCTCCAAAGACTGAAAGACTCTTCTGCTGAGCTTTATTCT 765
 QY 892 AATTGTGCTCGAAATTTCCGGTTCAGAGCTTTGAGCCCTTGAAGAAATCAACATC 951
 Db 766 AACTGTGTCGACGAACTTTCTGTTGCAAGCCCTTGAGATGCTTGAACACTTGGATGC 825
 QY 952 AAAATGATTCTTATGTGTGTTGTACAGGAACCGTGTGAAAGAGTGAACAAAGTGA 1011
 Db 826 AANAATGATTATATGTGTGTTGTCTGTAACCGTGAACGCAAGTGAACAAAGTGA 885
 QY 1012 GCCTGAGACATCAAAATTTAGCTTAGCTGTTTGAATAATTCGAATGAGGAAGTATGTA 1071
 Db 886 ACTTTGAAGCGCTACAGATTTCAGCTTGGCATTTTGAAGATTTCTAATGAGGAGTATGTA 945
 QY 1072 ACTGAAAAATTTCTCAATCCCTTGTGCTGGAACCTGCTGCTGTTGTTGTTGCTCCA 1131
 Db 946 ACTGAAAAATTTTTCAGTCACTAGTAGCAGGTTCTATTCCCGTGTGTTGTTGTTGCTCCA 1005
 QY 1132 AATATTGAGACTTTGCTCTCTCTCTGTTTCAATTTTACATATTAAGAGATAGAGGAT 1191
 Db 1006 AATATTCAAGATTTTCTCGGAGAGGCGCAATATTACATATTAAAGAGCTTGAT 1065
 QY 1192 GTTGAGTCTGTTGCAAGACCATGAGATATCTAGCAGAAAAATCCCGAAGCATATATCAA 1251
 Db 1066 GTTGCTTCACTGCTAAGACAAATGAAAAATTTTCTTCAACCTGATGCTTCAATCAA 1125
 QY 1252 TCATTGAGTGGAGATGAGGTCCATCTGACTCTTCAAGCCCTTGGGATATGGCA 1311
 Db 1126 TCTTTGAGTGGAGATGATGATGCTCCATCCGATTCTTTCAAGCTCTTATTGATCATGGCA 1185
 QY 1312 GCTGTGATTCATCTGCGCTGTTTTCATTTCACTTGGCCACAGTAGAGAGAGGAA 1371
 Db 1186 GCGGTTCAITTCATCTTGTGCTGTTTGTATACATATTGCTACCAAGATTCATTTAAAGGAG 1245
 QY 1372 GAAAAATAATCCAGCCCTTAAGACAGCTCTTGAAGTGCATAGAGGGCGCAGAAACCGTA 1431
 Db 1246 GAAAGGACTCCAAATTTACAAATCGTCTTGTAGCTGTTTCCACCAAAAGGGAACAATT 1305

QY 1432 TATCATATCTATGTCCAGAGAAAGGGAGGTTTGGATGAGTCCATTTTACCTGAGGTCT 1491
 Db 1306 TACCACCTTATTTATCCGAGAGAGAGGCGGTTTAACTCAGAGAGCATTTTACATGATCA 1365
 QY 1492 AGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTGTTTGAAGTTCACATCCCTGAAT 1551
 Db 1366 GGCAGTTAACTCTGGAGCCTTGGAAATCCGAGTCTCGTAAATTTAGGTCCCTCAAC 1425
 QY 1552 CTTGTCCTGTATGAGAGACTGAAAGGCTGAAGTTTAAAGAGGGGGAGTCTTTAAAA 1611
 Db 1426 CAGGTTCTGTATGGAAGATGAAAGGCCACCGAGCATTTAGAGTGGGATGACCTGAAA 1485
 QY 1612 CTCTACAAATATACCAATTTGCTTGACACAGAGCAAGCTCTTTATACCTTTCAGCTTC 1671
 Db 1486 TTATACAGATTTTACCAGTCCGTCTAACGCAACGTCAGCTTTGTACGTTTATGATTT 1545
 QY 1672 AAAGTGTGATGCTGATTTTCAGGAGTCACTTTGGAGAAACAATCTTTGTGCCCAAGTTGAAGTC 1731
 Db 1546 AGGGATGATTTCTGAACTCGAGCAATATATCAAAGACCATCCCTGTGCAAAAGCTTGAAGTA 1605
 QY 1732 ATTTTGTGTAGC 1744
 Db 1606 ATTTTGTGTAAAC 1618

RESULT 5

ACN54249
 ID ACN54249 standard; cDNA; 650 BP.
 XX ACN54249;
 XX AC
 XX 02-DEC-2004 (first entry)
 XX DE
 DE Cotton androecium tissue EST Clone ID: LIB3828-022-Q1-K6-F4, SEQ:9030.
 XX KW
 KW Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium;
 KW variety Nucotton33B; library LIB3828; molecular tag; molecular marker;
 KW genetic mapping; molecular mapping; seed germination; plant growth;
 KW plant quality; plant yield; plant breeding; tissue printing; ss.
 XX OS
 OS Gossypium hirsutum.
 XX PN
 PN US2004123340-A1.
 XX XX
 PD 24-JUN-2004.
 XX PF
 PF 12-DEC-2001; 2001US-00021323.
 XX PR
 PR 14-DEC-2000; 2000US-0255619P.
 XX PA
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 XX PI
 PI Deikman J, Feng PCC, Fincher KL, Ziegler TE;
 XX DR
 DR WPI; 2004-479808/45.
 XX PT
 PT New isolated nucleic acid molecule that encodes a plant protein or its
 PT fragment, useful for isolating a variety of agronomically significant
 PT genes associated with plant growth, quality or yield, and as molecular
 PT tags to map genes.
 XX PS
 PS Claim 1; SEQ ID NO 9030; 34pp; English.
 XX CC
 CC The invention relates to 17880 cotton expressed sequence tags (ESTs;
 CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
 CC from primed or non-primed seeds from variety DP50B, mature seeds from
 CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoeium
 CC tissue, developing fibres, carpel walls and septa from variety
 CC Nucotton33B. The invention also relates to substantially purified

CC	expression of foreign genes in plants	
XX		
SQ	Sequence 2165 BP; 664 A; 424 C; 345 G; 732 T; 0 U; 0 Other;	
	Query Match 9.5%; Score 209.4; DB 4; Length 2165;	
	Best Local Similarity 66.5%; Pred. No. 6.1e-45;	
	Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;	
QY	1486 AGGCTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTGTTTGAAGTTTCACATCC 1545	
DB		
	170 AGATCTAGCAATTTAACTCTGGAGTCTTCAAGACTGCTGTTCTTACGAAGTTTCAGTGCC 229	
QY	1546 CTGAATCTTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTTATTAAGAGGGGGAGTGT 1605	
DB		
	230 CTGAATCATGTTCTGTATGGAAGCCTGAAAGACCTCAAATTTAAAGGTGGCGATAAA 289	
QY	1606 TTAAACTCTACAAAATATACCAATTTGGCTTGACACAGACAGCAAGCTCTTTATACCTTC 1665	
DB		
	290 TTGAAGGTTTACAAAATATACCTCGCGGCTTGACACAGAGGCAAGCTCTTTATACCTTC 349	
QY	1666 AGCTTCAAAAGGTGATGCTGATTTTAACTGTTTAACTGTTTCTGTAGAAGTGCATAATCTTA 1725	
DB		
	1779 AGCTTCACTAGCTAGCACTAGCTAGAGTATTTAGGAATGAGTATGGCAGTGAATATGGC 1838	
QY	1726 GAAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778	
DB		
	410 GAAGTAAATTTTGTGTAGCATATGTTGAGCTACCTACAATTTACATGATCACCTAGCAT 469	
QY	1779 AGCTTCACTAGCTAGCACTAGCTAGAGTATTTAGGAATGAGTATGGCAGTGAATATGGC 1838	
DB		
	470 AGCTTCTTCACTTAACTGAGAGAAATGAAGTTTGTAGGAATGAGTATGACCATGGCGGC 529	
QY	1839 ATGGCTTT-----TATTTATGCTAGTCTTCTTGGCCAACTCAATTCATGATGTTT 1884	
DB		
	530 ATGGCTTTGTAATGCCCTACCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAT 589	
QY	1885 GTATAAGACATCACACTTTAACTTTAACTGTTTCTGTAGAAGTGCATAATCTTAATTTA 1944	
DB		
	590 ATACATGACTTCAACCATACCTTAAACCCCTTTTGTAGAATACTGAATGTTTCATATTTA 649	
QY	1945 ATGCTTAGTATTTAGTGTCTTATCTGATCATCT 1977	
DB		
	650 ATGTTGGGTTGTAGTGTGTTTACTTGATTATAT 682	
RESULT 9		
AAF84916		
ID	AAF84916 standard; DNA; 2232 BP.	
AC	AAF84916;	
XX		
DT	09-JUL-2001 (first entry)	
XX		
DE	Nitrogen-inducible promoter for regulating foreign gene expression.	
XX		
KW	nitrogen-inducible promoter; nitrite reductase gene; Nir gene;	
XX		
OS	Synthetic.	
XX		
PN	WO200125454-A2.	
XX		
PD	12-APR-2001.	
XX		
PP	02-OCT-2000; 2000WO-CA001143.	
XX		
PR	04-OCT-1999; 99US-0157133P.	
XX		
PA	(MEDI-) MEDICAGO INC.	
XX		
PI	Vezina L, D'aout M;	
XX		
DR	WPI; 2001-308228/32.	

XX	Regulating foreign gene transcription in transgenic plants, comprises transforming a plant (cell) with an expression construct having nitrogen-inducible promoter, an open reading frame of a gene and a polyadenylation site.
PT	
PT	
XX	Claim 1; Page 37-38; 44pp; English.
PS	
XX	AAF84905-17 represent nitrogen-inducible promoters. They are promoters of the nitrite reductase (Nir) gene. The promoter is used for regulating the foreign gene transcription in transgenic organisms. The method uses an expression construct having a nitrogen-inducible promoter, with(out) cis-acting sequence, operably linked to the gene to be expressed and modulated for transcriptional expression of the gene by addition or removal of a nitrogen inducer, an open reading frame of a gene, and a 3' polyadenylation signal. The method is useful for regulating the transcription of transgenes in genetically modified organisms. The nitrogen-inducible expression cassettes are useful for the controlling expression of foreign genes in plants
CC	
XX	Sequence 2232 BP; 686 A; 436 C; 362 G; 748 T; 0 U; 0 Other;
SQ	
	Query Match 9.5%; Score 209.4; DB 4; Length 2232;
	Best Local Similarity 66.5%; Pred. No. 6.2e-45;
	Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;
QY	1486 AGGCTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTGTTTGAAGTTTCACATCC 1545
DB	
	170 AGATCTAGCAATTTAACTCTGGAGTCTTCAAGACTGCTGTTCTTACGAAGTTTCAGTGCC 229
QY	1546 CTGAATCTTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTTATTAAGAGGGGGAGTGT 1605
DB	
	230 CTGAATCATGTTCTGTATGGAAGCCTGAAAGACCTCAAATTTCTAAAGGTGGCGATAAA 289
QY	1606 TTAAACTCTACAAAATATACCAATTTGGCTTGACACAGACAGCAAGCTCTTTATACCTTC 1665
DB	
	290 TTGAAGGTTTACAAAATATACCTCGCGGCTTGACACAGAGGCAAGCTCTTTATACCTTC 349
QY	1666 AGCTTCAAAAGGTGATGCTGATTTTAACTGTTTAACTGTTTCTGTAGAAGTGCATAATCTTA 1725
DB	
	1779 AGCTTCACTAGCTAGCACTAGCTAGAGTATTTAGGAATGAGTATGGCAGTGAATATGGC 1838
QY	1726 GAAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778
DB	
	410 GAAGTAAATTTTGTGTAGCATATGTTGAGCTACCTACAATTTACATGATCACCTAGCAT 469
QY	1779 AGCTTCACTAGCTAGCACTAGCTAGAGTATTTAGGAATGAGTATGGCAGTGAATATGGC 1838
DB	
	470 AGCTTCTTCACTTAACTGAGAGAAATGAAGTTTGTAGGAATGAGTATGACCATGGCGGC 529
QY	1839 ATGGCTTT-----TATTTATGCTAGTCTTCTTGGCCAACTCAATTCATGATGTTT 1884
DB	
	530 ATGGCTTTGTAATGCCCTACCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAT 589
QY	1885 GTATAAGACATCACACTTTAACTTTAACTGTTTCTGTAGAAGTGCATAATCTTAATTTA 1944
DB	
	590 ATACATGACTTCAACCATACCTTAAACCCCTTTTGTAGAATACTGAATGTTTCATATTTA 649
QY	1945 ATGCTTAGTATTTAGTGTCTTATCTGATCATCT 1977
DB	
	650 ATGTTGGGTTGTAGTGTGTTTACTTGATTATAT 682
RESULT 10	
AAF84906	
ID	AAF84906 standard; DNA; 2808 BP.
XX	
AC	AAF84906;
XX	
DT	09-JUL-2001 (first entry)
XX	
DE	Nitrogen-inducible promoter for regulating foreign gene expression.
XX	

KW nitrogen-inducible promoter; nitrite reductase gene; NiR gene;
 KW transgenic plant; transgene expression; ss.
 OS Synthetic.
 XX WO200125454-A2.
 XX 12-APR-2001.
 XX 02-OCT-2000; 2000WO-CA001143.
 XX 04-OCT-1999; 99US-0157133P.
 XX (MEDI-) MEDICAGO INC.
 XX Vezina L, D'aoust M;
 XX WPI; 2001-308228/32.
 XX Regulating foreign gene transcription in transgenic plants, comprises
 PT transforming a plant (cell) with an expression construct having nitrogen-
 PT inducible promoter, an open reading frame of a gene and a polyadenylation
 PT site.
 XX Claim 1; Page 29-30; 44pp; English.
 XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters of
 CC the nitrite reductase (NiR) gene. The promoter is used for regulating
 CC foreign gene transcription in transgenic organisms. The method uses an
 CC expression construct having a nitrogen-inducible promoter, with(out) cis-
 CC acting sequence, operably linked to the gene to be expressed and
 CC modulated for transcriptional expression of the gene by addition or
 CC removal of a nitrogen inducer, an open reading frame of a gene, and a 3'
 CC polyadenylation signal. The method is useful for regulating the
 CC transcription of transgenes in genetically modified organisms. The
 CC nitrogen-inducible expression cassettes are useful for the controlling
 CC expression of foreign genes in plants
 XX Sequence 2808 BP; 879 A; 502 C; 481 G; 946 T; 0 U; 0 Other;
 SQ Query Match 9.5%; Score 209.4; DB 4; Length 2808;
 Best Local Similarity 66.5%; Pred. No. 6.9e-45;
 Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;
 QY 1486 AGGCTAGCAATTTAACTCTGAATCTGTAAGGCTGCTGTTTGAAGTTACATCC 1545
 DB 909 AGATCTAGCAATTTAACTCTGAGTCTTCAAGACTGCTGTTTACGAAGTTACGTC 968
 QY 1546 CTGAATCTTGCTGCTGTAAGACTGAAAGGCTGAAAGTATTAAGAGGGGGAGTCT 1605
 DB 969 CTGAATCATGTTCTGTAAGGCTGAAAGACTCAAAATCTTAAAGGTTGGCGATAA 1028
 QY 1606 TTAAGAACTCTACAAATATACCAATTTGGCTTGACAGACAGCAAGCTCTTTATACCTTC 1665
 DB 1029 TTGAAGTTTACAAATATACCTCTGGGCTTGACAGAGGCAAGCTCTTTATACCTTC 1088
 QY 1666 AGCTTCAAGGTTGATGCTGATTTAGGAGTCACTTGGAGAACATCTTGCCAGTTT 1725
 DB 1089 CAGTTTCAAGCGGGATGTTGATTTCAAGTCTTGGAGAGCAATCTTGTGCGCAAGTTT 1148
 QY 1726 GAAGTCATTTTGTGTAGCATATGTTGAGCTACCTTACATTTACATGATCAGCTAGCT 1778
 DB 1149 GAAGTAAATTTTGTGTAGCATATGTTGAGCTACCTTACATTTACATGATCAGCTAGCT 1208
 QY 1779 AGCTTCACTTAGCTAGCACTAGTATGATTTTGAAGATGAGTATGGCAGTGAATATGCG 1838
 DB 1209 AGCTCTTTCACCTTAACTAGAGAACTAGTTTGAAGATGAGTATGACATGAGTGGGC 1268
 QY 1839 ATGGCTT-----TATTATGCGCTAGTTTCTTGGCCAACTCAATTTGATGTTT 1884
 DB 1269 ATGGCTTGTAAATGCTACCTTACTTTGGCCAACTCATCGGGGAATTTACATTTAGAAAAT 1328
 QY 1885 GTATAAGACATCACACTTTAACTTTTAACTTGTCTGTAGAGTGCATAATCCATATTA 1944

DB 1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTGAAGATAACTGAATGTTTATTTA 1388
 QY 1945 ATGCTTAGTTTCTAGTCTCTTATCTGATCATCT 1977
 DB 1389 ATGTTGGTGTGTAGTGTGTTTACTTGATATAT 1421
 RESULT 11
 AAF84909
 ID AAF84909 standard; DNA; 2863 BP.
 XX AAF84909;
 XX 09-JUL-2001 (first entry)
 XX Nitrogen-inducible promoter for regulating foreign gene expression.
 DE nitrogen-inducible promoter; nitrite reductase gene; NiR gene;
 KW transgenic plant; transgene expression; ss.
 XX Synthetic.
 XX WO200125454-A2.
 XX 12-APR-2001.
 XX 02-OCT-2000; 2000WO-CA001143.
 XX 04-OCT-1999; 99US-0157133P.
 XX (MEDI-) MEDICAGO INC.
 XX Vezina L, D'aoust M;
 XX WPI; 2001-308228/32.
 XX Regulating foreign gene transcription in transgenic plants, comprises
 PT transforming a plant (cell) with an expression construct having nitrogen-
 PT inducible promoter, an open reading frame of a gene and a polyadenylation
 PT site.
 XX Claim 1; Page 31-32; 44pp; English.
 XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters of
 CC the nitrite reductase (NiR) gene. The promoter is used for regulating
 CC foreign gene transcription in transgenic organisms. The method uses an
 CC expression construct having a nitrogen-inducible promoter, with(out) cis-
 CC acting sequence, operably linked to the gene to be expressed and
 CC modulated for transcriptional expression of the gene by addition or
 CC removal of a nitrogen inducer, an open reading frame of a gene, and a 3'
 CC polyadenylation signal. The method is useful for regulating the
 CC transcription of transgenes in genetically modified organisms. The
 CC nitrogen-inducible expression cassettes are useful for the controlling
 CC expression of foreign genes in plants
 XX Sequence 2863 BP; 890 A; 525 C; 485 G; 963 T; 0 U; 0 Other;
 SQ Query Match 9.5%; Score 209.4; DB 4; Length 2863;
 Best Local Similarity 66.5%; Pred. No. 7e-45;
 Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;
 QY 1486 AGGCTAGCAATTTAACTCTGAATCTGTAAGGCTGCTGTTTGAAGTTACATCC 1545
 DB 909 AGATCTAGCAATTTAACTCTGAGTCTTCAAGACTGCTGTTTCTACGAAGTTACGTC 968
 QY 1546 CTGAATCTTGCTGCTGTAAGACTGAAAGGCTGAAAGTATTAAGAGGGGGAGTCT 1605
 DB 969 CTGAATCATGTTCTGTAAGGCTGAAAGACTCAAAATCTTAAAGGTTGGCGATAA 1028
 QY 1606 TTAAGAACTCTACAAATATACCAATTTGGCTTGACAGACAGCAAGCTCTTTATACCTTC 1665
 DB 1029 TTGAAGTTTACAAATATACCTCTGGGCTTGACAGAGGCAAGCTCTTTATACCTTC 1088

QY	1666	AGCTTCAAAGGTGATGCTGATTTTCTGAGAGTCACTTGGAGAACAAATCCTTTGTGCCAAGTTT	1725
DB	1089	CAGTTCAAACGGGATGTTGATTTTCTGAGAGTCACTTGGAGAACAAATCCTTTGTGCCAAGTTT	1148
QY	1726	GAAGTCAATTTTGTAGCAATGGCTAA-----ATGGTACCTCTGCTTACCTCAATTT	1778
DB	1149	GAAGTCAATTTTGTAGCAATGGCTAA-----ATGGTACCTCTGCTTACCTCAATTT	1208
QY	1779	AGCTTCACTTAGCTAGCACTAGCTAGATTTTGAAGATGAGTATGCGAGTGAATATGGC	1838
DB	1209	AGCTTCTTCACTTAACCTAGAGAAATGAAGTTTGTAGGAATGAGTATGACCAATGAGTGGC	1268
QY	1839	ATGGCTT-----TATTTATGCTAGTTTCTTGGCAACTCATCGGGATTTACATTCAGAAAT	1884
DB	1269	ATGGCTTGTGAATGCTTACCTTGTGGCAACTCATCGGGATTTACATTCAGAAAT	1328
QY	1885	GTATAAGACATCACACTTTAAATTTTAACTGTTTCTGTAGAAAGTGCAAAATCATATTTTA	1944
DB	1329	ATACATGACTTCAACCATACTTAAACCCCTTTTGTAAAGATAACTGAATGTTTCATATTTA	1388
QY	1945	ATGCTTAGTTTGTAGTCTCTTATCTGATCATCT	1977
DB	1389	ATGTTGGTTGTAGTGTGTTTACTTGATTATAT	1421
RESULT 12			
AAF84912	AAF84912 standard; DNA; 2904 BP.		
ID	AAF84912	09-JUL-2001 (first entry)	
XX	AAF84912;	Nitrogen-inducible promoter for regulating foreign gene expression.	
XX	09-JUL-2001	nitrogen-inducible promoter; nitrite reductase gene; NiR gene;	
XX	Nitrogen-inducible promoter for regulating foreign gene expression.	transgenic plant; transgene expression; ss.	
XX	Synthetic.	Synthetic.	
XX	WO200125454-A2.	WO200125454-A2.	
XX	12-APR-2001.	12-APR-2001.	
XX	02-OCT-2000; 2000WO-CA001143.	02-OCT-2000; 2000WO-CA001143.	
XX	04-OCT-1999; 99US-0157133P.	04-OCT-1999; 99US-0157133P.	
XX	(MEDI-) MEDICAGO INC.	(MEDI-) MEDICAGO INC.	
XX	Vezina L, D'aoust M;	Vezina L, D'aoust M;	
XX	WPI; 2001-308228/32.	WPI; 2001-308228/32.	
XX	Regulating foreign gene transcription in transgenic plants, comprises transforming a plant (cell) with an expression construct having nitrogen-inducible promoter, an open reading frame of a gene and a polyadenylation site.	Regulating foreign gene transcription in transgenic plants, comprises transforming a plant (cell) with an expression construct having nitrogen-inducible promoter, an open reading frame of a gene and a polyadenylation site.	
XX	Claim 1; Page 34-35; 44pp; English.	Claim 1; Page 34-35; 44pp; English.	
XX	AAF84905-17 represent nitrogen-inducible promoters. They are promoters of the nitrite reductase (NiR) gene. The promoter is used for regulating foreign gene transcription in transgenic organisms. The method uses an expression construct having a nitrogen-inducible promoter, with(out) cis-acting sequence, operably linked to the gene to be expressed and modulated for transcriptional expression of the gene by addition or removal of a nitrogen inducer, an open reading frame of a gene, and a 3' polyadenylation signal. The method is useful for regulating the transcription of transgenes in genetically modified organisms. The nitrogen-inducible expression cassettes are useful for the controlling expression of foreign genes in plants	AAF84905-17 represent nitrogen-inducible promoters. They are promoters of the nitrite reductase (NiR) gene. The promoter is used for regulating foreign gene transcription in transgenic organisms. The method uses an expression construct having a nitrogen-inducible promoter, with(out) cis-acting sequence, operably linked to the gene to be expressed and modulated for transcriptional expression of the gene by addition or removal of a nitrogen inducer, an open reading frame of a gene, and a 3' polyadenylation signal. The method is useful for regulating the transcription of transgenes in genetically modified organisms. The nitrogen-inducible expression cassettes are useful for the controlling expression of foreign genes in plants	

PT Regulating foreign gene transcription in transgenic plants, comprises
 PT transforming a plant (cell) with an expression construct having nitrogen-
 PT inducible promoter, an open reading frame of a gene and a polyadenylation
 PT site.

XX Claim 1; Page 36-37; 44pp; English.

XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters of
 CC the nitrite reductase (Nir) gene. The promoter is used for regulating
 CC foreign gene transcription in transgenic organisms. The method uses an
 CC expression construct having a nitrogen-inducible promoter, with(out) cis-
 CC acting sequence, operably linked to the gene to be expressed and
 CC modulated for transcriptional expression of the gene by addition or
 CC removal of a nitrogen inducer, an open reading frame of a gene, and a 3'
 CC polyadenylation signal. The method is useful for regulating the
 CC transcription of transgenes in genetically modified organisms. The
 CC nitrogen-inducible expression cassettes are useful for the controlling
 CC expression of foreign genes in plants

XX Sequence 2971 BP; 925 A; 549 C; 508 G; 989 T; 0 U; 0 Other;

Query Match 9.5%; Score 209.4; DB 4; Length 2971;
 Best Local Similarity 66.5%; Pred. No. 7.1e-45;
 Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy	1486	AGGCTAGCAATTTAACTCTGAAGCTGCTGAGGCTGCTGTTTGAAGTTCACATCC	1545
Db	909	AGATCTAGCAATTTAACTCTGAGCTCTTCAAGACTGCTGTTTACGAAGTTCACGTC	968
Qy	1546	CTGAATCTTGCTGCTGATGAAGACTGAAAGGCTGAAAGTATAAGAGGGGGAGTCT	1605
Db	969	CTGAATCATGTTCTGATGAAGCTGAAAGACTCAAAATCTTAAAGGTGGCGATAA	1028
Qy	1606	TTAAAGCTTCAAAATATACCAATGCTGTGACAGACAGCAAGCTCTTTATACCTTC	1665
Db	1029	TTGAAGGTTTTACAAATATACCTCGCGGCTTGACACAGAGCGCAAGCTCTTTATACCTTC	1088
Qy	1666	AGCTTCAAGGTGATGCTGATTTTCAAGGAGTCACTTGGAGAGCAACTCTTGCCAAAGTTT	1725
Db	1089	CAGTTCAACGGGATGTTGATTTTCAAGGAGTCACTTGGAGAGCAACTCTTGCCAAAGTTT	1148
Qy	1726	GAAGTCAATTTTGTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT	1778
Db	1149	GAAGTAAATTTTGTGTAGCATGTTGAGTACCTTACATTTACATGATCATTGACAT	1208
Qy	1779	AGCTTCACTTACCTAGCTAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT	1838
Db	1209	AGCTCTTTTCACTTAACTAGAGAAATGAAGTTTGAAGTATGAGTATGAGTATGAGT	1268
Qy	1839	ATGGCTT-----TATTTATGCTAGTATTTCTTGGCCAACTCATTTGATGTTT	1884
Db	1269	ATGGCTTTGTAATGCTACCTACTTTGGCCAACTCATCGGGGATTTTACATTCAGAAA	1328
Qy	1885	GTATAAGACATCACACTTTAAATTTTAACTTGTCTGTAGAAGTGCATATTTA	1944
Db	1329	ATACATGACTTCAACCATTTAAACCCCTTTTGTAGATTAAGTATGATTTTATTTA	1388
Qy	1945	ATGCTTTAGTTTGTAGTCTTCTTCTGATCATCT 1977	
Db	1389	ATGTTGGGTGTAGTGTGTTTACTTGAATATAT 1421	

RESULT 14

ID AAF84905 standard; DNA; 3714 BP.

XX AAF84905;

XX 23-JUL-2001 (first entry)

DE Nitrogen-inducible promoter for regulating foreign gene expression.

XX nitrogen-inducible promoter; nitrite reductase gene; Nir gene;

KW transgenic plant; transgene expression; ss.
 XX Synthetic.
 OS WO200125454-A2.
 XX 12-APR-2001.
 XX 02-OCT-2000; 2000WO-CA001143.
 XX 04-OCT-1999; 99US-0157133P.
 XX (MEDI-) MEDICAGO INC.
 XX Vezina L, D'aoust M;
 XX WPI; 2001-308228/32.
 XX Regulating foreign gene transcription in transgenic plants, comprises
 PT transforming a plant (cell) with an expression construct having nitrogen-
 PT inducible promoter, an open reading frame of a gene and a polyadenylation
 PT site.
 XX Claim 1; Page 28-29; 44pp; English.
 XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters of
 CC the nitrite reductase (Nir) gene. The promoter is used for regulating
 CC foreign gene transcription in transgenic organisms. The method uses an
 CC expression construct having a nitrogen-inducible promoter, with(out) cis-
 CC acting sequence, operably linked to the gene to be expressed and
 CC modulated for transcriptional expression of the gene by addition or
 CC removal of a nitrogen inducer, an open reading frame of a gene, and a 3'
 CC polyadenylation signal. The method is useful for regulating the
 CC transcription of transgenes in genetically modified organisms. The
 CC nitrogen-inducible expression cassettes are useful for the controlling
 CC expression of foreign genes in plants

XX Sequence 3714 BP; 1166 A; 645 C; 649 G; 1254 T; 0 U; 0 Other;

Query Match 9.5%; Score 209.4; DB 4; Length 3714;
 Best Local Similarity 66.5%; Pred. No. 7.9e-45;
 Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy	1486	AGGCTAGCAATTTAACTCTGAAGCTGCTGAGGCTGCTGTTTGAAGTTCACATCC	1545
Db	909	AGATCTAGCAATTTAACTCTGAGCTCTTCAAGACTGCTGTTTACGAAGTTCACGTC	968
Qy	1546	CTGAATCTTGCTGCTGATGAAGACTGAAAGGCTGAAAGTATAAGAGGGGGAGTCT	1605
Db	969	CTGAATCATGTTCTGATGAAGCTGAAAGACTCAAAATCTTAAAGGTGGCGATAA	1028
Qy	1606	TTAAAGCTTCAAAATATACCAATGCTGTGACAGACAGCAAGCTCTTTATACCTTC	1665
Db	1029	TTGAAGGTTTTACAAATATACCTCGCGGCTTGACACAGAGCGCAAGCTCTTTATACCTTC	1088
Qy	1666	AGCTTCAAGGTGATGCTGATTTTCAAGGAGTCACTTGGAGAGCAACTCTTGCCAAAGTTT	1725
Db	1089	CAGTTCAACGGGATGTTGATTTTCAAGGAGTCACTTGGAGAGCAACTCTTGCCAAAGTTT	1148
Qy	1726	GAAGTCAATTTTGTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT	1778
Db	1149	GAAGTAAATTTTGTGTAGCATGTTGAGTACCTTACATTTACATGATCATTGACAT	1208
Qy	1779	AGCTTCACTTACCTAGCTAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT	1838
Db	1209	AGCTCTTTTCACTTAACTAGAGAAATGAAGTTTGAAGTATGAGTATGAGTATGAGT	1268
Qy	1839	ATGGCTT-----TATTTATGCTAGTATTTCTTGGCCAACTCATTTGATGTTT	1884
Db	1269	ATGGCTTTGTAATGCTACCTACTTTGGCCAACTCATCGGGGATTTTACATTCAGAAA	1328
Qy	1885	GTATAAGACATCACACTTTAAATTTTAACTTGTCTGTAGAAGTGCATATTTA	1944

Db	1329	ATACATGACTTCACCATACCTTAAACCCCTTTTCTGAAGATAAAGTAATGTTTCATATTTA	1388
QY	1945	ATGCTTAGTCTTGTAGTCTTATCTGATCATCT	1977
Db	1389	ATGTTGGGTTGAGTGTCTTTTACTTGATATAT	1421
RESULT 15			
AD38881	AAD38881 standard; DNA; 3775 BP.		
XX	AC	AAD38881;	
XX	DT	23-SEP-2002 (first entry)	
XX	DE	Alfalfa AP2 adaptor with nitrite reductase gene (Nir) promoter.	
XX	XX	Expression regulatory sequence; recombinant polypeptide; gene cloning;	
KW	alfalfa; nitrite reductase gene; Nir; AP2 adaptor; ds.		
XX	OS	Medicago sativa.	
XX	PN	WO200236786-A2.	
XX	PD	10-MAY-2002.	
XX	PF	31-OCT-2001; 2001WO-CA001532.	
XX	PR	31-OCT-2000; 2000US-0244214P.	
XX	PA	(MEDI-) MEDICAGO INC.	
XX	PI	Vezina L, D'aoust M, Arcand F, Bilodeau P;	
XX	DR	WPI; 2002-471503/50.	
XX	PT	Isolating and characterizing an expression regulatory sequence for	
PT	oligonucleotide primers that amplify sequences upstream or downstream of		
PT	CDNAs.		

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Job time : 1228 secs

Example 2; Page 67-68; 74pp; English.

The invention relates to a method for isolating and characterising an expression regulatory sequence for the expression of recombinant polypeptides and/or RNA. The method comprising producing at least one oligonucleotide primer from cDNAs of a cDNA library, where the oligonucleotide primer allows amplification of genomic sequences upstream or downstream of the cDNAs. The method is useful for isolating, characterising and identifying a large number of known and unknown promoters that are active under any desired environmental condition to which a cell may be exposed and not just to the exemplified isolation of promoters that are capable of expression in specific conditions. The methods are also useful for cloning genes from any host, or from a specific tissue with such host, from which a cDNA library may be constructed; for the identification and isolation of analogous promoters, signal peptides and structural genes in several species of multicellular and unicellular organisms and as a high throughput identification system of candidate therapeutic targets. The promoter sequences may be used to regulate the synthesis of polypeptides. The present sequence is alfalfa AP2 adaptor with nitrite reductase gene (Nir)

Sequence 3775 BP; 1180 A; 658 C; 670 G; 1267 T; 0 U; 0 Other;

Query Match	9.5%;	Score 209.4;	DB 6;	Length 3775;
Best Local Similarity	66.5%;	Pred. No. 8e-45;		
Matches	341;	Conservative 0;	Mismatches 151;	Indels 21; Gaps 2;
QY	1486	AGGCTAGCAATTTAACTCTGAAGCTGCTGTTGTTTGAAGTTCACATCC	1545	
Db	957	AGATCTAGCAATTTAACTCTGGAGTCTCTTCAAGACTGCTGTTTACGAAGTTCACGTCC	1016	
QY	1546	CTGAATCTTGTGCTGTATGAAGACTGAAAGGCTGGAAGTTATAGAGGGGGAGTGCT	1605	

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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9792.182 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Maximum Match 0%
Listing first 45 summaries

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9: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209.4	9.5	2069	3	US-09-678-300-3
2	209.4	9.5	2124	3	US-09-678-300-6
3	209.4	9.5	2165	3	US-09-678-300-9
4	209.4	9.5	2232	3	US-09-678-300-12
5	209.4	9.5	2808	3	US-09-678-300-2
6	209.4	9.5	2863	3	US-09-678-300-5
7	209.4	9.5	2904	3	US-09-678-300-8
8	209.4	9.5	2971	3	US-09-678-300-11
9	209.4	9.5	3714	3	US-09-678-300-1
10	47.8	2.2	1141	3	US-09-806-708B-22
11	44.4	2.0	1639	2	US-08-737-524B-1
12	43.6	2.0	1141	3	US-09-806-708B-22
13	42.6	1.9	1055	3	US-09-806-708B-23
14	42.4	1.9	662	3	US-08-998-416-185
15	42.4	1.9	665	3	US-08-998-416-937
16	42.4	1.9	701	3	US-08-998-416-701
17	42.4	1.9	711	3	US-08-998-416-786
18	42.4	1.9	724	3	US-08-998-416-683
19	42.4	1.9	732	3	US-08-998-416-1036
20	42.4	1.9	828	3	US-08-998-416-538
21	42.4	1.9	834	3	US-08-998-416-305
22	42	1.9	663	3	US-08-998-416-191
23	42	1.9	860	3	US-08-998-416-287
24	41.6	1.9	832	3	US-09-621-976-2813

c 25	41.4	1.9	200663	3	US-09-949-016-12569	Sequence 12569, A
c 26	41.4	1.9	203093	3	US-09-949-016-14445	Sequence 14445, A
c 27	40.6	1.8	7218	3	US-08-232-463-14	Sequence 14, Appl
c 28	40.6	1.8	9027	3	US-09-949-016-11883	Sequence 11883, A
c 29	40.6	1.8	9027	3	US-09-949-016-17574	Sequence 17574, A
c 30	40.4	1.8	854	3	US-08-998-416-534	Sequence 534, App
c 31	40.2	1.8	1274	3	US-09-270-767-10133	Sequence 10133, A
c 32	40.2	1.8	42923	3	US-09-949-016-17307	Sequence 17307, A
c 33	39.6	1.8	3715	3	US-09-234-245-1	Sequence 1, Appli
c 34	39.4	1.8	3573	3	US-09-353-585-4	Sequence 4, Appli
c 35	39	1.8	601	3	US-09-949-016-126020	Sequence 126020, A
c 36	39	1.8	74790	3	US-09-949-016-15321	Sequence 15321, A
c 37	38.8	1.8	2523	3	US-09-861-451A-29	Sequence 29, Appl
c 38	38.6	1.8	6124	3	US-08-213-419B-3	Sequence 3, Appli
c 39	38.6	1.8	69199	3	US-09-949-016-13881	Sequence 13881, A
c 40	38.6	1.8	150394	3	US-09-949-016-13042	Sequence 13042, A
c 41	38.2	1.7	7218	2	US-08-232-463-14	Sequence 14, Appl
c 42	38.2	1.7	36154	3	US-09-949-016-13190	Sequence 13190, A
c 43	38	1.7	1454	2	US-08-220-958-3	Sequence 3, Appli
c 44	38	1.7	2428	3	US-09-731-166-5	Sequence 5, Appli
c 45	38	1.7	4298	3	US-09-724-857-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-678-300-3
; Sequence 3, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'Aoust, Marc-Andr,
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-3

Query Match	9.5%;	Score	209.4;	DB	3;	Length	2069;
Best Local Similarity	66.5%;	Pred. No.	1.5e-50;				
Matches	341;	Conservative	0;	Mismatches	151;	Indels	21;
Gaps	2;						
Qy	1486	AGGCTAGCAATTTAACTCTGAAGCTGCTGAAGCTCTGTTGTTTGAAGTTCACATCC	1545				
Db	170	AGATCTAGCAATTTAACTCTGAGTCTCTCAAGACTCTGTTTACGAAGTTCACGTC	229				
Qy	1546	CTGAATCTTGCTGCTATGGAAGCTGAAGGCTCAAGTTATAAGAGGGGAGTGCT	1605				
Db	230	CTGAATCATGTTCTCTGATGGAAGCTCAAGTCTCAATTTCAAAGGTGGCGATAA	289				
Qy	1606	TAAAACTCTACAAAATATACCCAAATTTGGCTTGACAGAGACAAGCTCTTTATACCTTC	1665				
Db	290	TTGAAGGTTTACAAAATATACCCCTCGCGGCTTGACAGAGACAAGCTCTTTATACCTTC	349				
Qy	1666	AGCTTCAAAGGTGATGCTGATTTTCAAGAGTCATCTTGAGAGACAATCTTTGCGCAAGTTT	1725				
Db	350	CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAGCAATCTTTGCGCAAGTTT	409				
Qy	1726	GAAGTCATTTTGTGTAGTAGCGCTAA-----ATGGTACCTCTCTCTACCTGAATT	1778				

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Db      410 GAAGTAATTTTGTGTAGCATATGTTAGCTACCTACCAATTTACATGATCACCTAGCAAT 469
Qy      1779 AGCTTCACTAGCTAGCACTAGCTAGAGTTTGTAGGAATGAGTATGGCAGTGAATATGCG 1838
Db      470 AGCTCTTTTCACTAACTGAGAGAAATGAAGTTTGTAGGAATGAGTATGACCATGGAGTCGGC 529
Qy      1839 ATGGCTT-----TATTTATGCGCTAGTGTCTTGGCCAACTCAATGATGTTTT 1884
Db      530 ATGGCTTTGTAATGCTACCCCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAT 589
Qy      1885 GTATAAGACATCACACTTTAAATTTTAAACTTGTCTGTAGAGTGCATAATCCATATTTA 1944
Db      590 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGATAAATGAATGTTTATATTTA 649
Qy      1945 ATGCTTAGTTTATGCTCTTATCTGATCATCT 1977
Db      650 ATGTTGGGTTGTAGTGTTTTACTTGATTATAT 682

RESULT 2
US-09-678-300-6
; Sequence 6, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'Aoust, Marc-Andr  
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-6

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Query Match          9.5%; Score 209.4; DB 3; Length 2124;
Best Local Similarity 66.5%; Pred. No. 1.5e-50;
Matches 341; Conserved 0; Mismatches 151; Indels 21; Gaps 2;

Qy      1486 AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTTGAAGTTTCAATCC 1545
Db      170 AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGTTTACGAAGTTTCACTGCC 229
Qy      1546 CTGAATCTTGTGCTGTATGGAAGCTGAAAGGCTCAAGTTATAGAGGGGGAGTGCT 1605
Db      230 CTGAATCATGTTCTGTATGGAAGCTGAAAGGCTCAAAATCTTAAAGGTGGCGATAAA 289
Qy      1606 TTAATACTCTACAAAATATACCAATTTGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1665
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Qy      1666 AGCTTCAAAAGGTGATGCTGATTTAGAGTCACTTGGAGAGCAATCTTGTGCGCAAGTTT 1725
Db      350 CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAGCAATCTTGTGCGCAAGTTT 409
Qy      1726 GAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778
Db      410 GAAGTAATTTTGTAGCATATGTTGAGCTACTCAATTTACATGATCACCTAGCAAT 469
Qy      1779 AGCTTCACTAGCTAGCACTAGCTAGAGTTTGTAGGAATGAGTATGGCAGTGAATATGCG 1838
Db      470 AGCTTCACTTAACTGAGAGATGAAGTTTGTAGGAATGAGTATGAGTATGAGTATGAGTATG 529
Qy      1839 ATGGCTT-----TATTTATGCGCTAGTGTCTTGGCCAACTCAATGATGTTTT 1884
Db      530 ATGGCTTTGTAATGCGCTACCCCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAT 589
Qy      1885 GTATAAGACATCACACTTTAAATTTTAAACTTGTCTGTAGAGTGCATAATCCATATTTA 1944

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Qy      1839 ATGGCTT-----TATTTATGCGCTAGTGTCTTGGCCAACTCAATGATGTTTT 1884
Db      530 ATGGCTTTGTAATGCGCTACCCCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAT 589
Qy      1885 GTATAAGACATCACACTTTAAATTTTAAACTTGTCTGTAGAGTGCATAATCCATATTTA 1944
Db      590 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGATAAATGAATGTTTATATTTA 649
Qy      1945 ATGCTTAGTTTATGCTCTTATCTGATCATCT 1977
Db      650 ATGTTGGGTTGTAGTGTTTTACTTGATTATAT 682

RESULT 3
US-09-678-300-9
; Sequence 9, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'Aoust, Marc-Andr  
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-9

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Query Match          9.5%; Score 209.4; DB 3; Length 2165;
Best Local Similarity 66.5%; Pred. No. 1.5e-50;
Matches 341; Conserved 0; Mismatches 151; Indels 21; Gaps 2;

Qy      1486 AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTTGAAGTTTCAATCC 1545
Db      170 AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGTTTACGAAGTTTCACTGCC 229
Qy      1546 CTGAATCTTGTGCTGTATGGAAGCTGAAAGGCTGAAAGGCTTATAAGAGGGGGAGTGCT 1605
Db      230 CTGAATCATGTTCTGTATGGAAGCTGAAAGGCTCAAAATCTTAAAGGTGGCGATAAA 289
Qy      1606 TTAATACTCTACAAAATATACCAATTTGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1665
Db      290 TTGAAGGTTTACAAAATATACCTTGGGGCTTGACACAGAGCAAGCTCTTTATACCTTC 349
Qy      1666 AGCTTCAAAAGGTGATGCTGATTTAGAGTCACTTGGAGAGCAATCTTGTGCGCAAGTTT 1725
Db      350 CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAGCAATCTTGTGCGCAAGTTT 409
Qy      1726 GAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778
Db      410 GAAGTAATTTTGTAGCATATGTTGAGCTACTCAATTTACATGATCACCTAGCAAT 469
Qy      1779 AGCTTCACTAGCTAGCACTAGCTAGAGTTTGTAGGAATGAGTATGGCAGTGAATATGCG 1838
Db      470 AGCTTCACTTAACTGAGAGATGAAGTTTGTAGGAATGAGTATGAGTATGAGTATGAGTATG 529
Qy      1839 ATGGCTT-----TATTTATGCGCTAGTGTCTTGGCCAACTCAATGATGTTTT 1884
Db      530 ATGGCTTTGTAATGCGCTACCCCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAT 589
Qy      1885 GTATAAGACATCACACTTTAAATTTTAAACTTGTCTGTAGAGTGCATAATCCATATTTA 1944

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Db 590 ATACATGACTTCAACCATACTCTTAAACCCCTTTTGTGAAGATAACTGAATGTTCATATTTA 649

Qy 1945 ATGCTTAGTTTTAGTGCCTCTTATCTGATCACT 1977

Db 650 ATCTGGGTTGTAGTGTCTTTTACTTGATTATAT 682

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RESULT 4
US-09-678-300-12
; Sequence 12, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'AOUT, Marc-Andr,
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; TITLE OF INVENTION: FOREIGN GENES
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678, 300
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/157,133
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2232
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for r
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-12

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RESULT 5
US-09-678-300-2
; Sequence 2, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'ACOSTA, Marc-Andr,
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; TITLE OF INVENTION: FOREIGN GENES
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/157,133
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2808
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for r
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-2

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RESULT 6
US-09-678-300-5
; Sequence 5, Application US/09678300
; Patent No. 6420548

Fri Feb 24 14:58:34 2006

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; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'AOUST, Marc-Andr  
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; TITLE OF INVENTION: FOREIGN GENES
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2863
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-5

Query Match          9.5%; Score 209.4; DB 3; Length 2863;
Best Local Similarity 66.5%; Pred. No. 1.8e-50;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTAACCTGTAAGTCTGTAAGGCTGCTGTTTGAAGTTTCAATCC 1545
Db 909 AGATCTAGCAATTAACCTGTAAGTCTGTAAGGCTGCTGTTTGAAGTTTCAATCC 968
QY 1546 CTGAATCTTGCTGCTGTAAGTCTGTAAGGCTGTAAGGCTGTAAGGCTGTAAGGCTGCT 1605
Db 969 CTGAATCTTGCTGCTGTAAGTCTGTAAGGCTGTAAGGCTGTAAGGCTGTAAGGCTGCT 1028
QY 1606 TTAAACTCTACAAAATATACCAATTTGGCTTTGACACAGAGCAAGCTCTTTATACCTTC 1665
Db 1029 TTGAAGTTTACAAAATATACCTCGGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1088
QY 1666 AGCTTCAAAAGGTGATGCTGTAATTTAGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 1725
Db 1089 CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 1148
QY 1726 GAAGTCATTTTGTGTAGCATATGTTAGCTTACCTCAATTTACATGATCACCTAGCAIT 1778
Db 1149 GAAGTAAATTTTGTGTAGCATATGTTAGCTTACCTCAATTTACATGATCACCTAGCAIT 1208
QY 1779 AGCTTCACTTAGCTAGCACTAGCTAGAGTATTTAGGAATGAGTATGGCAGTGAATATGGC 1838
Db 1209 AGCTTCACTTAGCTAGCACTAGCTAGAGTATTTAGGAATGAGTATGGCAGTGAATATGGC 1268
QY 1839 ATGGCTT-----TATTTATGCTAGTCTTCTTATCTGATCATCT 1884
Db 1269 ATGGCTTGTAAATGCTACCTACTTTGGCCAACTCATCGGGGATTTACATTCAGAAAT 1328
QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTGTTTCTGTAGAAGTCAAAATCCATATTTA 1944
Db 1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAAAGTAACTGAATGTTTCAATATTA 1388
QY 1945 ATGCTTAGTTTGTAGTCTCTTATCTGATCATCT 1977
Db 1389 ATGTTGGTGTAGTGTGTTTACTTGAATATAT 1421

RESULT 7
US-09-678-300-8
; Sequence 8, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'AOUST, Marc-Andr  
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; TITLE OF INVENTION: FOREIGN GENES
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-8

Query Match          9.5%; Score 209.4; DB 3; Length 2904;
Best Local Similarity 66.5%; Pred. No. 1.8e-50;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTAACCTGTAAGTCTGTAAGGCTGCTGTTTGAAGTTTCAATCC 1545
Db 909 AGATCTAGCAATTAACCTGTAAGTCTGTAAGGCTGCTGTTTGAAGTTTCAATCC 968
QY 1546 CTGAATCTTGCTGCTGTAAGTCTGTAAGGCTGTAAGGCTGTAAGGCTGTAAGGCTGCT 1605
Db 969 CTGAATCTTGCTGCTGTAAGTCTGTAAGGCTGTAAGGCTGTAAGGCTGTAAGGCTGCT 1028
QY 1606 TTAAACTCTACAAAATATACCAATTTGGCTTTGACACAGAGCAAGCTCTTTATACCTTC 1665
Db 1029 TTGAAGTTTACAAAATATACCTCGGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1088
QY 1666 AGCTTCAAAAGGTGATGCTGTAATTTAGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 1725
Db 1089 CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 1148
QY 1726 GAAGTCATTTTGTGTAGCATATGTTAGCTTACCTCAATTTACATGATCACCTAGCAIT 1778
Db 1149 GAAGTAAATTTTGTGTAGCATATGTTAGCTTACCTCAATTTACATGATCACCTAGCAIT 1208
QY 1779 AGCTTCACTTAGCTAGCACTAGCTAGAGTATTTAGGAATGAGTATGGCAGTGAATATGGC 1838
Db 1209 AGCTTCACTTAGCTAGCACTAGCTAGAGTATTTAGGAATGAGTATGGCAGTGAATATGGC 1268
QY 1839 ATGGCTT-----TATTTATGCTAGTCTTCTTATCTGATCATCT 1884
Db 1269 ATGGCTTGTAAATGCTACCTACTTTGGCCAACTCATCGGGGATTTACATTCAGAAAT 1328
QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTGTTTCTGTAGAAGTCAAAATCCATATTTA 1944
Db 1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAAAGTAACTGAATGTTTCAATATTA 1388
QY 1945 ATGCTTAGTTTGTAGTCTCTTATCTGATCATCT 1977
Db 1389 ATGTTGGTGTAGTGTGTTTACTTGAATATAT 1421

RESULT 8
US-09-678-300-11
; Sequence 11, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'AOUST, Marc-Andr  
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; TITLE OF INVENTION: FOREIGN GENES
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-8
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SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 11
LENGTH: 2971

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Sequences to be used as promoter for regulating

OTHER INFORMATION: expression of foreign genes

US-09-678-300-11

Query Match 9.5%; Score 209.4; DB 3; Length 2971;

Best Local Similarity 66.5%; Pred. No. 1.8e-50;

Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

1486 AGGCTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTTGAAGTTTCACATCC 1545

909 AGATCTAGCAATTTAACTCTGGAGTCTTCAAGACTGCTGTTCTTACGAAGTTTCAGTCC 968

1546 CTGAATCTTTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTTATAGAGGGGGAGTGTCT 1605

969 CTGAATCATGTTCTGTATGGAAGCTGAAAGACCTCAAAATCTTAAAGGTGGCGATAA 1028

1606 TTAAGAACTCTACAAAATATACCAATTTGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1665

1029 TTGAAGGTTTACAAAATATACCTCGGGCTTGACACAGAGGCAAGCTCTTTATACCTTC 1088

1666 AGCTTCAAGGTTGATGCTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGTGCAAGTTT 1725

1089 CAGTTCAAGGGGATGTTGATTTTCAAGACTGCTTGGAGCAATCTTGTGCAAGTTT 1148

1726 GAAGTCATTTTGTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778

1149 GAAGTAAATTTTGTGTAGCATATGTTGAGTACCTACCAATTTACATGATCACCTAGCAT 1208

1779 AGCTTCACCTAGCTAGACTAGTATAGTATTTAGGAATGAGTATGGCAGTGAATATGCG 1838

1209 AGCTCTTTCACCTTAACTGAGAGAAATGAAGTTTTTGGCAACTCATCGGGATTTACATCAGAAAAT 1268

1839 ATGGCTT-----TATTTATGCTAGTTTCTTGGCAACTCATCGGGATTTACATCAGAAAAT 1884

1269 ATGGCTTTGTAATGCTACCTACTTTGGCAACTCATCGGGATTTACATCAGAAAAT 1328

1885 GTATAAGACATCACACTTTAAATTTTAACTTGTCTGTAGAAGTCAAAATCCATATTTA 1944

1329 ATACATGACTTCAACACTACTTAAACCCCTTTTGAAGTAACGAAATGTTTCATATTTA 1388

1945 ATGCTTAGTTTATGCTCTTATCTGATCATCT 1977

1389 ATGTTGGGTTGATGTTTCTTACTTGATTATAT 1421

RESULT 9

US-09-678-300-1

Sequence 1, Application US/09678300

Patent No. 6420548

GENERAL INFORMATION:

APPLICANT: VOZINA, Louis-Philippe

APPLICANT: D'Aoust, Marc-Andr,

APPLICANT: MEDICAGO INC.

TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF

FILE REFERENCE: 14149-3"PCP"

CURRENT APPLICATION NUMBER: US/09/678,300

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: US 60/157,133

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 3714

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

Query Match

Best Local Similarity 2.2%; Score 47.8; DB 3; Length 1141;

Matches 68; Conservative 255; Mismatches 335; Indels 0; Gaps 0;

OTHER INFORMATION: Sequences to be used as promoter for regulating

OTHER INFORMATION: expression of foreign genes

US-09-678-300-1

Query Match

Best Local Similarity 9.5%; Score 209.4; DB 3; Length 3714;

Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

1486 AGGCTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTTGAAGTTTCACATCC 1545

909 AGATCTAGCAATTTAACTCTGGAGTCTTCAAGACTGCTGTTCTTACGAAGTTTCAGTCC 968

1546 CTGAATCTTTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTTATAGAGGGGGAGTGTCT 1605

969 CTGAATCATGTTCTGTATGGAAGCTGAAAGACCTCAAAATCTTAAAGGTGGCGATAA 1028

1606 TTAAGAACTCTACAAAATATACCAATTTGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1665

1029 TTGAAGGTTTACAAAATATACCTCGGGCTTGACACAGAGGCAAGCTCTTTATACCTTC 1088

1666 AGCTTCAAGGTTGATGCTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGTGCAAGTTT 1725

1089 CAGTTCAAGGGGATGTTGATTTTCAAGACTGCTTGGAGCAATCTTGTGCAAGTTT 1148

1726 GAAGTCATTTTGTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778

1149 GAAGTAAATTTTGTGTAGCATATGTTGAGTACCTACCAATTTACATGATCACCTAGCAT 1208

1779 AGCTTCACCTAGCTAGACTAGTATAGTATTTAGGAATGAGTATGGCAGTGAATATGCG 1838

1209 AGCTCTTTCACCTTAACTGAGAGAAATGAAGTTTTTGGCAACTCATCGGGATTTACATCAGAAAAT 1268

1839 ATGGCTT-----TATTTATGCTAGTTTCTTGGCAACTCATCGGGATTTACATCAGAAAAT 1884

1269 ATGGCTTTGTAATGCTACCTACTTTGGCAACTCATCGGGATTTACATCAGAAAAT 1328

1885 GTATAAGACATCACACTTTAAATTTTAACTTGTCTGTAGAAGTCAAAATCCATATTTA 1944

1329 ATACATGACTTCAACACTACTTAAACCCCTTTTGAAGTAACGAAATGTTTCATATTTA 1388

1945 ATGCTTAGTTTATGCTCTTATCTGATCATCT 1977

1389 ATGTTGGGTTGATGTTTCTTACTTGATTATAT 1421

RESULT 10

US-09-806-708B-22

Sequence 22, Application US/09806708B

Patent No. 6784342

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

FILE REFERENCE: 4810-58741

CURRENT APPLICATION NUMBER: US/09/806,708B

CURRENT FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/147,133

PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.0

SEQ ID NO 22

LENGTH: 1141

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY: promoter

LOCATION: (1)..(1141)

OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters

Query Match

Best Local Similarity 10.3%; Pred. No. 0.0029;

Matches 68; Conservative 255; Mismatches 335; Indels 0; Gaps 0;

[illegible]

RESULT 11
US-08-737-524B-1
; Sequence 1, Application US/08737524B
; Patent No. 5912414
; GENERAL INFORMATION:
; APPLICANT: CARL SAVERIO FALCO
; APPLICANT: DOMINICK ANTHONY GUIDA, JR.
; APPLICANT: MARY ELIZABETH HARNETT LOCKE
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS, CHIMERIC
; TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
; TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEEDS
; TITLE OF INVENTION: OF PLANTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,524B
; FILING DATE:

```

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1059-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..1441
US-08-737-524B-1

Query Match      2.0%; Score 44.4; DB 2; Length 1639;
Best Local Similarity 55.1%; Pred. No. 0.036;
Matches 87; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy      2041  CACTCAGACACATATTACTTCATGTTGGTTTTCATGATCATCGAGCTTTTTTAGTGTCTG 2100
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1446  CACTCTAATCAGTTTGTATTTCACAAATCATGAGTGATGCGTCTCTTGGATCTTTGCAA 1505
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2101  GAACTGTCCTCTGGTTTGGACACCTGTTATTGCTTCAGTGTATTCTCCAGTGGTTATC 2160
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1506  GATCTGTGACAATCATATGACCTGATGATGCGAATAAGTTCTCTTTTCTTTATTC 1565
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2161  GTTTTGGACCTCTAAAAAaaaaaaaaaaaaaaaaaaaaa 2198
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1566  CGTCAAATTCAAAAAaaaaaaaaaaaaaaaaaaaaa 1603
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 12
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

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	Query Match	2.0%;	Score 43.6;	DB 3;	Length 1141;
	Best Local Similarity	11.3%;	Pred. No. 0.049;		
	Matches 117;	Conservative 357;	Mismatches 555;	Indels 4;	Gaps 2;
Qy	1160	GTTCAAATTTACATATATAAAGACATGAGGATGTTGAGTCTGTTGCAAGACCATGAGAT	1219		
Db	1132	GNTTTTKTKYKANNNNNNNGHKDWRMDATKWSATGTAWWNTHAKRGATCMCYWYWT	1073		
Qy	1220	ATCTAGCAGAAATCCCGAAGCATATAATCAATTCATTGAGGTGGAAGTATGAGGGTCCAT	1279		
Db	1072	GTNRRCMRTYAMRTYTRSNANWSCATKEHWNTMKKYATKYRTAWYAMWCARWNNMWC	1013		


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QY 1280 CTGACTCTTCAAGCCCTTGTGATATGCGAGCTGTGCTATTCATCGTGGCTTTGCA 1339
Db 1012 ATNGTAKSCATNNMTATTRWAAYAAKWARHAGNNRMWYGAAGKNGOMAMATMGB 953
QY 1340 TTCACCTGGCCACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1399
Db 952 WADTAGKMCNNNNNNNTDVRMMAMKAKNNNNNNAVWTCYNRAATNNKMAITHMKWTH 893
QY 1400 CTTGCAAGTGCATAGAGGGCCAGAAACCGTATATCATATCTATGTCAGAGAAAGGGA 1459
Db 892 GAHSKRTRHTRTCRTKYNNNNNNNARTVYVYHHAARRWNNNAWTRTNNNNNNNNNAC 833
QY 1460 GGTGTTGAGAGTCCATTACCTGAGGCTACCAATTTAACTCTCAATGCTGCTGAAG 1519
Db 832 RNTRT---WWABVHSHSCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 776
QY 1520 CTGCTGTGTTTGAAGTTCACATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1579
Db 775 CNYMHAATVTHTDWCYKTMNTWYWDMTTMBTTTTTRNMTTSTNNNNNNNNNNNNNN 716
QY 1580 CTGAAGTTATAAGAGGGGAGTCTTTAACTCTACAAATATATCCCAATGCTGCTGA 1639
Db 715 NNNNNMKAYYAHATNNWGWNTDARTNNNTVMRRRWNTNKTWYSTTRHHYTG 656
QY 1640 CACAGACAGCTCTTTATACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1699
Db 655 TNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 596
QY 1700 -TGAGAACAACTCTGTCGCAAGTGTGAAGTCAATTTTGTGTAGCATGGCTAAATGGT 1758
Db 595 VWYVAMRCBDVTYTRNNYCKSYAHYVWVSNAMWYRYSARNSMARWTRNNWW 536
QY 1759 ACCTCTCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1818
Db 535 MSGBVRMRWAGTMMRRHNNNTDTRYVWVWKRWBTTTVYDSMCAKSMWRGNRRAM 476
QY 1819 AGTATGCGAGTGAATGCGATGCTTTATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1878
Db 475 KMMVAAANDAGMDHWTYMGNNMMRRRAKMMMAWCRAYCCNNNNNNRACVWHKHM 416
QY 1879 TGTTTGTATAAGACATCACACTTTAAATTTTAACTGTTTCTCTAGAAGTGCATAATCCA 1938
Db 415 WRWTWKYWKAAACNNNBKAMVAMVSRDNTNDMMWTSDBWHWYVVDYTWRA 356
QY 1939 TATTTAATGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1998
Db 355 WNNNNNNNRBCKTTSWMMHDMHNTCTYGNNTWGSAYBMAAMSMMAAGASNBVTYNWC 296
QY 1999 TTGTGAGTGAACACTGAACTTAATAGAGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCT 2058
Db 295 WRMTYMGKTMNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 236
QY 2059 ACTTCATGTTGTTGATGATGCTGAGCTTTTGTAGTCTGGAAGTCTGCTGCTGCTGCTT 2118
Db 235 MGKHHBWRABHRSNNMMWVCKRYVSWHWHAMRYBKABAVGNNNNWKRMAHH 176
QY 2119 GAGCACCTGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2178
Db 175 WCATNNNNMMWYVYMHMHKHKGAATNNNTABRDDHBAHVKTWYVRYDWCAMCWN 116
QY 2179 AAAAAAAAAAAAAA 2191
Db 115 AKAKVRTAMKHW 103

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RESULT 13
 US-09-806-708B-23/c
 ; Sequence 23, Application US/09806708B
 ; Patent No. 6784342
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of British Columbia
 ; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

; FILE REFERENCE: 4810-58741
 ; CURRENT APPLICATION NUMBER: US/09/806,708B
 ; CURRENT FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/147,133
 ; PRIOR FILING DATE: 1999-08-04
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 1055
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; NAME/KEY: promoter
 ; LOCATION: (1)..(1055)
 ; OTHER INFORMATION: consensus sequence of A.t. and L.a. PAB1 promoters
 US-09-806-708B-23

Query Match 1.9%; Score 42.6; DB 3; Length 1055;
 Best Local Similarity 18.6%; Pred. No. 0.092;
 Matches 84; Conservative 129; Mismatches 239; Indels 0; Gaps 0;

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QY 1575 AAGCCCTGAAGTTATTAAGAGGGGAGTGTCTTTAAACTCTACAAATATATCCCAATGG 1634
Db 477 AAGGYMRAAWAGTWMAAMANNNTTRTYAWWTRWARYTTTRYRSACNAKSMWRGATWRA 418
QY 1635 CTTGACACAGACAGACAGCTCTTTATACCTTCAGCTTCAAAGGTGATGCTGATTTTCAGGAG 1694
Db 417 ATMTTAAANKAGAWMMWTTAAGNTWTAAATATMAAAWCAAYCCNNNNWAAACMAKMKM 358
QY 1695 TCACCTTGGAGAACAACTCTTGTGCAAGTTTGAAGTCAATTTTGTGTAGCATGGCTTAAA 1754
Db 357 WAMTWKYAWGAAACNNNNKTAMYCRRAMWYSAWTTTWWAAATSWWKWYTTTRKTMTAAA 298
QY 1755 TGGTACCTCTGCTCTACCTGAAATAGCTTCACTAGCTAGCTAGCTAGCTAGCTAGCTAG 1814
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QY 1815 AATGAGTATGCGAGTGAATATGCGATGCTTTTATTTATGCTAGTCTTCTTGGCCAACTCA 1874
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QY 1875 TTGATGTTTGTATAAGACATCACACTTTAAATTTTAACTGTTTCTGTAGAAGTGCATA 1934
Db 177 WYBARAAYVATCTWSTCRWKTARGWVYAMRYTWAKASGCGNNNAKWRCAWYACATN 118
QY 1935 TCATATTTAATGCTGCTAGTTTGTGCTCTTATCTGATCATCTAGAAGTCACTGTTCTTG 1994
Db 117 NNAMAWYACAYWYTAGKAAWNTNNKTASGKMMYAMMKTTWYWAYWTCACAMWATAKRR 58
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Db 57 TAAKMCWYTRGYMCANNNGRRWAMCAACMAA 26

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RESULT 14
 US-08-998-416-185
 ; Sequence 185, Application US/08998416
 ; Patent No. 6239264
 ; GENERAL INFORMATION:
 ; APPLICANT: Philippsen, Peter
 ; APPLICANT: Pohlmann, Rainer
 ; APPLICANT: Steiner, Sabine
 ; APPLICANT: Mohr, Christine
 ; APPLICANT: Wendland, Jorgen
 ; APPLICANT: Knechtle, Philipp
 ; APPLICANT: Reibschung, Corinne
 ; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
 ; AND USES THEREOF
 ; NUMBER OF SEQUENCES: 1152
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: NO. 6239264artis Corporation
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park

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OM nucleic - nucleic search, using sw model
Run on: February 19, 2006, 15:45:58 ; Search time 2476 Seconds
(without alignments)
7340.910 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1284.8	58.5	2177	7	US-10-424-599-94124
2	664.8	30.2	2036	8	US-10-739-930-1070
3	657	29.9	1790	7	US-10-425-114-33374
4	657	29.9	1962	8	US-10-425-115-63646
5	561	25.5	1713	7	US-10-437-963-81205
6	327.4	14.9	1056	8	US-10-425-115-11856
7	273.6	12.4	887	7	US-10-437-963-81203
8	245.2	11.2	650	7	US-10-021-323-9030
9	244.8	11.1	853	8	US-10-425-115-63643
10	176.4	8.0	553	7	US-10-424-599-64336
11	145.8	6.6	567	7	US-10-021-323-7941
12	144	6.6	554	7	US-10-437-963-19720
13	110.8	5.0	812	8	US-10-425-115-63644
14	108.4	4.9	466	8	US-10-425-115-112285
15	86.8	3.9	860	8	US-10-425-115-172748
16	86.2	3.9	810	7	US-10-425-114-27910
17	84.2	3.8	287	3	US-09-294-0938-5780
18	75.4	3.4	279	7	US-10-424-599-24082
19	68.4	3.1	271	7	US-10-424-599-71566
20	61.2	2.8	236	7	US-10-424-599-3541
21	58.6	2.7	954	7	US-10-424-599-123113
22	50.6	2.3	1538	7	US-10-437-963-5998
23	50.2	2.3	509	7	US-10-424-599-63519
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					Sequence 1070, Ap
					Sequence 33374, A
					Sequence 63646, A
					Sequence 81205, A
					Sequence 11856, A
					Sequence 81203, A
					Sequence 9030, Ap
					Sequence 63643, A
					Sequence 64336, A
					Sequence 7941, Ap
					Sequence 19720, A
					Sequence 63644, A
					Sequence 112285, A
					Sequence 172748, A
					Sequence 27910, A
					Sequence 5780, Ap
					Sequence 24082, A
					Sequence 71566, A
					Sequence 3541, Ap
					Sequence 123113, A
					Sequence 5998, Ap
					Sequence 63519, A

ALIGNMENTS

RESULT 1
US-10-424-599-94124
; Sequence 94124, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 94124
; LENGTH: 2177
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56005C.1
US-10-424-599-94124

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Best Local Similarity	83.5%	Pred. No.	0;				
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Gaps	12;						
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QY	161	CTTTGATT-TTTTAGT	TTATTTTTCGGAATTCGGAGTTCGGGGCGCAATTTGATGATGGT	219			
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QY	220	CTGTTGAGATCTTC	GAGGCTCGAGACAGATGGT-CCCAACAAGACAGCTTACCC	276			
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QY	277	GTTT-----TGG	CTCGGAGGCAACCCAAAGAGGAATGGAGCAATCTAATGCTCTTTGT	332			
Db	350	GTCTTCGCGGTTT	CCGAGTTCGCTCCGAGAGGAATGGACCAATCTAATGCAAGCTGG	409			
QY	333	TGTTGCCCTT--	GTGGTCAATCGCGAGA-TGCGTTTCTGGGTAGGTGGATATGCGCA	389			
Db	410	TCGTGCGCCTAG	TGCTGTTGCGGAGAGTCCGTTTTCTCGGAGGCTCGACATGCGCA	469			

Fri Feb 24 14:58:34 2006

us-09-913-858c-1.rnpbm

QY 652 GATGCCGCAATTTGGGTTTACCTCAACCAAGTGGAAACAGCTAGCATTTCTCGATCAATGGAA 711
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QY 526 GATGCTACATTTGGGAATTCACACAGATCTTCTGTAGATGGTATCTCTCAGATCAATGGAA 585
Db |||||
QY 712 TCAGCAGAAATCTATGCTGAGAACAAATATTCGCATGGCAAGCAGGGGATATAACATC 771
Db |||||
QY 586 TCATCTCAATATTAATTCAGAAATAATATTTGATGTGGCTCGAGGGAGGGGTACAAAGATT 645
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QY 772 GTAATGACACAGCTATCTTCGATGTTCTGCTTTGGGATATTTTTCATGGGCTCAGTAT 831
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QY 646 GTGATGACACACAGCTTCTTCAGACGATCCAGTTGGCTACTTTTCATGGGCTGAAAT 705
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QY 832 GATATGATGGCACACAGTCAGCGCGAAATCTGAAGCTGCTTCTGACGCTGCTTTTCATTTCC 891
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QY 706 GATATCATGGCACCTGTGCTCCAAAGACTGAAGAAGCTCTTGTGCGAGCCCTTATTTCT 765
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QY 892 AATTTGGTGTGCGAAATTTCCGTTTGAAGCTCTTGAAGCCCTTGAAAAATCAACATC 951
Db |||||
QY 766 AACTGTGGTGCAGAACTTTCTGTTTGAAGCCCTTGAGATGCTTTGAAAACTTGGATGTC 825
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QY 1012 GCCTGAAGCAGCTACAAATTTAGCTTAGCGTTTGAAAAATTCGAAATGAGGAAGATTATGTA 1071
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QY 1432 TATCATATCTATGTACAGAAAGGGGAAGTTTGAAGTGGAGTCCATTTTACCTTCAAGTCT 1491
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QY 1492 AGCAATTTACTCTGAATGCTGTGAAGCTGCTGTTGTTTGAAGTTTCAATCCCTCAAT 1551
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QY 1552 CTTGTGCTGTATGGAAGACTGAAAGGCTTGAAGTTTATAGAGGGGGGAGTGTCTTTAAAA 1611
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QY 1546 AGGGATGATTTCTGAACCTCGAGCAATATATCAAGACCATCCCTGTGCAAGCCTTGAAGTA 1605
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QY 1732 ATTTTGTGTAGC 1744

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RESULT 4
US-10-425-115-63646
; Sequence 63646, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 63646
; LENGTH: 1962
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_158045C.1
US-10-425-115-63646
Query Match 29.9%; Score 657; DB 8; Length 1962;
Best Local Similarity 66.3%; Pred. No. 2.2e-170;
Matches 964; Conservative 0; Mismatches 480; Indels 9; Gaps 1;
QY 301 AAGAGAAATGAGCAATCTAATGCTCTTGTGTTGGTTCATCGCGAGATC 360
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QY 301 AGCGCGCGTGGGGGTGCTTCTCGCGCTCTCTGTGGCGCCCTTCTCGCCGAGATC 360
Db |||||
QY 361 GGGTTCTCGGGTAGTGTGATATGCAAAAAACGCGCCATCGTTGACTCCCTCGCTGAC 420
Db |||||
QY 361 GGGTTCTCGCGCGCTCGACATGGGAAGACGCGGCGGTGAGAGCTGGACACC 420
Db |||||
QY 421 TTCTTCTACCGTCTCGAGCGGTGTGAAGGTGACGATTTGGGGTGGGTTGGTGGCT 480
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QY 421 TCTTTTACCGCGCTCCCGCATTTGGCGCATGCGGTTGGGGGGCGCAGCCTCGAGG 480
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QY 481 TCTGATCGGAATCTGAAATCGTATAGT-----TGTGAGGAATGTTGGAGAGGAG 531
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QY 481 GCAGCGCGCGACAGCGGAGGACGAAGAGATCCGGCTGTGCGAGCGGCTCGAGAGGAG 540
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QY 601 AAGGATGGAAATAAATGCTACGTAGGATGTGAATTTGGT-----TGTGCGAGTAAGACACCT 660
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QY 661 GATGCTACATTTTGGAAATTTGACCAAGATCTCTTGTAGATGGTATCTCTCAGATCAATGAA 720
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QY 772 GTAATGACAAACCAAGTCTATCTTCGGATGTTCTCGTGTGGATATTTTTCATGGGCTGAGTAT 831
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901 AACTGTGGTGCAGAAACTTTTCGTTTGCAGCCCTTGAGATGCTTGAAAACTTGATGATGC 960
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1072 ACTGAAAAATTCCTCCAAATCCCTTGTGCTGGAATCTGCTCCCTGCTGTTGTTGGTCTCCA 1131
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1432 TATCATATCTATGTGAGAGAAAGGGAGGTTTGAGATGAGTCCATTTACCTGAGTCT 1491
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1492 AGCAATTTAATCTGATGCTGTGAGAGGCTGCTGTTGTTTGAAGTTTACATCCCTGAT 1551
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1552 CTCTGCTGTATGGAAGACTGAAAGGCTGAAAGTTTATAAGAGGGGGAGTGTCTTAAAA 1611
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1621 TTATACAGAAATTTACCCAGTCCGCTTAACGCAACGTCAGGCTTTGTACGGTTTATAGATT 1680
1672 AAAGGTGATGCTGATTTCCAGAGTCACTTGGAGACATCTTGTGCAAGTGTGGAAGTC 1731
1681 AGGATGATTTCTGAATCTGAGCAATATATCAAGACCATCCCTGTGCAAGAGCTTGAAGTA 1740
1732 ATTTTGTGTAGC 1744
1741 ATTTTGTGTAAAC 1753

RESULT 5
US-10-437-963-81205
; Sequence 81205, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81205
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_80755C.1
; US-10-437-963-81205

Query Match 25.5%; Score 561; DB 7; Length 1713;
Best Local Similarity 67.6%; Pred. No. 7.9e-144;
Matches 829; Conservative 0; Mismatches 350; Indels 48; Gaps 1;
Qy 564 AGAGCCTATTTTGTGTTCTGAGCTGATCAGGAGTGAAGTCGTGTTGGTGGATGTA 623
Db 486 AGAGCTACTTTTGGACTGTCTCAGCTCAACAGGATTTGAATAAATGTTCTGTAGGATGTA 545
Qy 624 ATTTGGGTTTAGTGGGATAGAAAGCCAGATGCCGATTTGGGTTACTCTCAACCAAGTGG 683
Db 546 ATTTGGGTTTTCAGTACTAAGCGCTGATCTACTTTTGGAAATGCCCCAGATCTTAC 605
Qy 684 AACAGCTAGCATTTCTGCGATCAATGGAATCAGCAGAAATCTATGCTGAGAACAAATATGTC 743
Db 506 TGTAGAGATCTCTCAGATCGATGGAGTCACTCTCAGTATTTATTCAGAGAACAAATATGTC 665
Qy 744 CATGGCAAGACGGAGGGGATATAACATCGTAAATGACAAACAGTCTATCTCGGATGTTCC 803
Db 666 TGTGGCTCGAGGGAGAGGTTACAAAATGTGATGACAAACAGCCTTTCTCAGATGTACC 725
Qy 804 TGTGGATATTTTTCATGGCTGAGTATGATATGATGATGATGATGATGATGATGATGATGAT 863
Db 726 TGTGGCTACTTTTCATGGCTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 785
Qy 864 AGCTGCTCTTGCAGCTGCTTTTCAATTTGGTGTCTGCAAAATTTCCGTTTGCAGAC 923
Db 786 AGAGCCCTAGCTGCAGCAATTTATTTCAACTGTGGTGCAGTAAATTTTCGTTTGCAGAC 845
Qy 924 TCTTGAGGCCCTTGAAAAATCAAAACATCAAAATTTGATTTCTTATGGTGGTGTGTCACAGAA 983
Db 846 CTTTGAGATGCTTGAGAGCTTAGATGTCAAAATTTGATTCATATGATGATGATGATGATGAT 905
Qy 984 CCGTATGAGAGTGAACAAAGTGAAGCCCTCAAGCACTACAAAATTTAGCTTAGCCTT 1043
Db 906 TCATGATGGCAAGTTGATAAAGTGGAAACTTTGAAGCGCTACAAAATTTAGCTTAGCCTT 965
Qy 1044 TGAATAATCGAATGAGGAAGATTATGTAACCTGAAAAAATTTCTTCAATCCCTTTGTGCTGG 1103
Db 966 TGAGAAATCCACGAGGAGATTTATGTTACAGAAAGTTTTTTTCAATCGCTGTTAAACAGG 1025
Qy 1104 AACTGTCCTGTGGTGTGTTGGTGTCTCAAAATATTTCAGAGCTTTGCTCTCTCTCTGTTTC 1163
Db 1026 AGCTATTTCCAGTTGTGATTTGGTCTCCAAAACATTTCAAGAGTTCTCTCTCTGGAGAGGCGC 1085
Qy 1164 AATTTTACATATTAAGAGATAGAGGATTTGAGTCTGTTGCAAGACCATGAGATATCT 1223
Db 1086 AATATTACATTAAGAGCTTTGATGATTTTCTTCAATTTGCCAAGACAAATGAACAATAT 1145
Qy 1224 AGCAGAAAAATCCGGAAGCATATAATCAATCAATGAGGTGGAAGTATGAGGCTCCATCTGA 1283
Db 1146 TGCATCAANTCAGGAAGCCTTTAATCAATCTTTGAGATGGAAGTATGATGGCCCATCTGA 1205
Qy 1284 CTCCTTCAAGGCCCTTTGAGATATGGCAGCTGTGCAATTCATCGTGGCGCTTTTGGATTC 1343
Db 1206 TTTCTTTCAAGGCCCTTTATGACATGGCAGCGGTTCAATTCATCATGTCTCTCTTGCATACA 1265
Qy 1344 CTTGGCCACAGTGTAGTAGAGAGGAAGAAAATTAATCCAGCCTTAAGAGACGCTTCTTGG 1403
Db 1266 TGTGCGCAGGAAGATTTCATGAGAAAGGAAAGGACCAACCAAAATTTTATGAATCGCCCATG 1325

[illegible]

```

RESULT 6
US-10-425-115-11856
; Sequence 11856, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 11856
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_11080C.1
US-10-425-115-11856

Query Match      14.9%; Score 327.4; DB 8; Length 1056;
Best Local Similarity 74.5%; Pred. No. 2.8e-79;
Matches 412; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY      709 GAATCAGCAGAACTACTATGCTGAGAACAAATATTTGCCATGCGAAGCGAGGGGATATAAC 768
      |||
Db      413 GAACCAATGTTCTATTGGTCTGGCAATTTCAITTGCTTTCTATACAGGAGAGGGTACAAG 472

QY      769 ATCGTAATGACACACGAGTCTATCTTCGGATGTTTCCTGTGGATATATTTTCATCGGCTGAG 828
      |||
Db      473 ATTGTGATGACAACACGACCTTTCTTCAGACGTACCGATTGGCTACTTTTCATGSGCTGAA 532

QY      829 TATGATATGATGGCCACGAGTGCAGCCGAAAACTGAAGCTGCTCTTTCAGCTGCTTTTCATT 888
      |||
Db      533 TATGATATCATGCGACCTGTGCTGCCCTCCAAAGACTGAAGAAGCTCTTGTGTCAGGCTTTATT 592

QY      889 TCCAATGTGGTCTGGAATTTCCGGTGTCCAAGCTCTTCAGGCGCCCTTGAAAAATCAAC 948
      |||
Db      593 TCTAACTGTGGTGACGAAACTTTCGTTTGCAAGCCCTTGAGATGCTTTGAAAACCTGGAT 652

QY      949 ATCAAAATTCATTCTTTATGGTGGTTGTTCACAGGAACCGTGTATGGAAGAGTGGAACAAAGTG 1008

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[illegible]

Query Match	12.4%;	Score 273.6;	DB 7;	Length 887;	
Best Local Similarity	66.0%;	Pred. No. 2e-64;			
Matches 396;	Conservative	0;	Mismatches 204;	Indels	0; Gaps 0
432	CTCTCGAGCGTCGTTGAAGGTGACGATTTGGGGTTGGGTTTGGGCTTCTGATCGGAA	491			
288	CCCCGGCGGACCGGGACGCGCCCCCGGGCGGAGGTGAGGTGGTGAGGAGGACGA	347			
492	TTCTGAATCGTATAGTTGTGTGAGGAATGGTTGTGAGAGGAGGAATGCTGTCACTATTCGAG	551			
348	CGGCGACATCCGGTTGTTCGAGGAGAGCGGCTTTGAGAGGAGGACGCGGTGCCGACGACCG	407			
552	GGGCTTTTCCAAAGAGCCGCTATTTTGTCTTGGAGCTCATCAGGAGTGGAAAGTCGTGTTC	611			
498	CGACTTCGACAGGATCCGTCCTCGTGGGGCGCCGCTAAGGATTGGAATAAATGTC	467			
612	GTTTCGGATGTAAATTGTTGGTTTGTGGGGATAGAAAGCCAGATCCGCAATTTGGGTACC	671			
468	TGTTAGGATGTGAATTTGGTTTTCAGCTACTAAGACGCTGATGCTACTTTTGGAAATGCG	527			
672	TCAACCAAGTGGAAACAGCTAGCATTTCTCGATTCAAATGGAATCAGCAGAAATCATGCTGA	731			


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Qy 708 GGAATCAGCAGATACTATGCTGAGAACAAATATTCCTCATGTCGACGAGCGGAGATATA 767
Db 512 GGAATCAGCAGATACTATGCTGAGAACAAATATTCCTCATGTCGACGAGCGGAGATATA 562
Qy 768 CATCGTAATGACAACAGCTCTATCTTCGAGATGTTCTCTGAGATATTTTTCATGGGCTGA 827
Db 563 -----GATGTCACAGTTGGCTACTTCTTTTCATGGGCTGA 594
Qy 828 GTATGATATGATGGACACAGTCGACCGGAAACTGAAGCTGCTCTTCGAGCTGCTTTTCAT 887
Db 595 ATATGATATCATGGACACCTGCTGCTCCAAAGACTGAAGAGCTCTGCTGAGACCTTTAT 654
Qy 888 TTCCAAATGCTGCTCGAAATTTCCGGTTGCAAGCTCTTCGAGGCCCTTGAAAAATCAAA 947
Db 655 TTCTAACTGCTGTCACGGAACCTTCGGTTTGAAGCCCTTGAGATGCTTNGAATAATTGGA 714
Qy 948 CATCAAAATTTGATTTTATGCTGTTGTCACAGGAACCGTGATGGAAGTGCAACAAAT 1007
Db 715 TGTCAAAATAGATTTCATATGCTAGTTGTTCATCGTAACCGTGATGGAAGTGCAACAAAT 774
Qy 1008 GGAAGCCCTGAACACTACAAATTTAGCTTAGCGTTTGAATTCGAATGAGGAAGATTA 1067
Db 775 GGACACCTTGAAGCGCTACAGATTACGCTTGGGCATTTGAGAANTTCTATGAGGAGGATA 834
Qy 1068 TGTAACTGAAAAATCTT 1085
Db 835 CGTAACAGAAAAATTTTT 852

RESULT 10
US-10-424-599-64336/c
; Sequence 64336, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 7941
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3828-022-Q1-N6-F4
US-10-021-323-7941

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Query Match 8.0%; Score 176.4; DB 7; Length 553;
Best Local Similarity 66.7%; Pred. No. 1.2e-37;
Matches 284; Conservative 0; Mismatches 136; Indels 6; Gaps 2;

Qy 1537 TTCATCCCTGAATCTTGCTGATGGAAGCTGAAAGCCCTGAAGTTATAAGAGGG 1596
Db 550 TCCCAACCCCGAATCCAGGCCCAAGGGGAAGCCAAAGAGCCCTCAANATTTTAAAGG 491
Qy 1597 GGGAGTCTTTAAACCTCAAAAATATACCAATTCGCTTGACACAGAGACCAAGCTCTT 1656
Db 490 GGCCATGATTTAAACCCCAATATAACCCCGTGGGTGACCCCAAAACCAAGCTTTT 431
Qy 1657 TATACCTTCAGCTTCAAGGTGATGCTGATTTTCAAGAGTCACTTGGAGAACATCTTGT 1716
Db 430 TAACCTTCGCTTCCAGGGAGGCGGATTTTCAAGGCTCCCTTGGAAACCCCCCTTGG 371
Qy 1717 GCCAAGTTGAAGTCATTTTGTAGCATGCGCTTAATGCTACCTCTGCTCTACCTGAA 1776
Db 370 GCAAGTTTGAAGTCATTTTGTAGCATGCGC-----AAGGGGCCCTCTGCTCCCCNAG 314

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Qy 1777 TTAGCTTCACTTAGCTAGCAGCTAGTAGAGTTTTCAGCAATGAGTATGCGCAGTGAATATG 1836
Db 313 AAAAGCTTTTCCCTTAACCTGACCGGGAAGATTTTGGGATGAGTATGCGCATGAAACTG 254
Qy 1837 GCATGGCTTTATTTATGCTAGTTTCTTGGCCAACTCATTTGATGATTTTGTATAGACATC 1896
Db 253 GCCGGGCTTTTATGCAAAAGCTTTTGGCCCCCTTGTATGATTTATATTCCAAATA 194
Qy 1897 ACATTTAAATTTAAACTTTTCTG---TAGAAGTGAATCCATATTTAAATGCTTAGT 1953
Db 193 AAATTTCTTTTGAACCTTTTGGGGCCAAAGGGGGGTTCCCCCATTTTAAAGCTTAGT 134
Qy 1954 TTTAGT 1959
Db 133 TTTAGT 128

RESULT 11
US-10-021-323-7941/c
; Sequence 7941, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 7941
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3828-022-Q1-N6-F4
US-10-021-323-7941

```

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Query Match 6.6%; Score 145.8; DB 7; Length 567;
Best Local Similarity 69.5%; Pred. No. 3.8e-29;
Matches 212; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

Qy 1439 TCTATGTCAGAGAAAGGGGAGGTTTGAGATGGAGTCCATTTACCTGAGGT-CTAGCAAT 1497
Db 566 TATACGTACGAGAACGAGGGAGGTTTAGATGGAATCTATTTTAAAGGTCGGGGAAT 507
Qy 1498 TTAACCTGTAATGCTGTAAGGCTGCTGTTTGTGAAGTTCACATCCCTGGAATCTGTG 1557
Db 506 ATGACCTTAAAGGCCCTTGAGGCTGCCGTTTCACACGATTTCAAGTTTCGAAACAGGTT 447
Qy 1558 CCTGTATGAGAGCTCAAAAGGCTGAAGTTATAAGAGGGGGGAGTGTCTTTTAAACCTCTAC 1617
Db 446 CCTATTGGAACCCGGAAGGCCAGAAAGCCCTTCGAGGTGGAGATGAATCAAAAGTATAC 387
Qy 1618 AAAATATACCAATTTGGCTTTGACACAGAGACAGCTCTTTTATACCTTCAGCTTCAAGGT 1677
Db 386 AGATATATCTCTTGGGTTGACACAAAGACAGGCTTTATATACATTTCAAGTTCAAGGG 327
Qy 1678 GATGCTGATTTAGGAGTCACTTGGAGAACATCTTGTGCGCAAGTTTGAAGTCATTTT 1737
Db 326 GATGCTGATCTTAAAGAACCATATATCGAAACCAACCCCTTGGCGGAAGTTTCGAAGTCTATTC 267
Qy 1738 GTGTA 1742
Db 266 GTGTA 262

RESULT 12
US-10-437-963-19720/c

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; FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_158043C.1
US-10-425-115-63644

Query Match          5.0%; Score 110.8; DB 8; Length 812;
Best Local Similarity 54.2%; Pred. No. 2.3e-19;
Matches 257; Conservative 0; Mismatches 202; Indels 15; Gaps 1;

Qy 303 GAGGAAATGGAGCAATCTAATGCCTCTTGTGTTGGCCCTTGTGCTCATCGCGGAGATCGC 362
Db      |||||
Qy 229 GCGCGATGGAGGTGCTTGTGCGCTCCTCGTAGGCGCCGCTTCTCTCGCGAGATCGC 288
Db      |||||
Qy 363 GTTCTTGGGTAGGTGGATATGGCCAAAACGCCGCCATGTTGACTCTCCTCGCTGACTT 422
Db      |||||
Qy 289 CTTCTCTGGCGCCCTCGACATGGCGAAGAACGCCGAGGTGGTCGAGAGCTGGACACCTC 348
Db      |||||
Qy 423 CTTCTACCGCTC-----TCGAGCGGTCTGTTCAAGGTGACGATTTTGGGGTT 467
Db      |||||
Qy 349 CTTTATCGCGCTCCTCCCATTTGGGTGAATCCGTGGGCGGGCGGGTCCCGAGGCG 408
Db      |||||
Qy 468 GGGTTTGGTGGCTTCTGATCGGAATCTGAATCGTATAGTTGTGAGGAATGTTGGAGAG 527
Db      |||||
Qy 409 AGACGGCGACGGCGACGCGAGGACGAAGAGATCCGGCGGTGCGAGCAGCGCTCGAGAG 468
Db      |||||
Qy 528 GGAGATGCTGTACAGTATTCGAGGGGCTTTTCCAAAGAGCCTATTTTGTTCCTGGAGC 587
Db      |||||
Qy 469 GGAGGACGGCTGCGCTTACGACCGCAGCTTTGACAGGAGTCCCGTGTCTGCGTGGGCG 528
Db      |||||
Qy 588 TGATCAGGCTGGAAGTCGTCTCGGTGGATGTAAATTTGGGTTTGTAGTGGGATAGAAA 647
Db      |||||
Qy 529 TGCCAAGGACTGGAGTAAATGCTATGAGGATGTCAAATTTGGTTTTCTGCCAGTAAGAC 588
Db      |||||
Qy 648 GCCAGATGCCGCATTTGGGTTTACCTCAACCAAGTGAACAGCTAGCATTTCTGCCGATCAAT 707
Db      |||||
Qy 589 ACCTGATGCTACTTTTGGAAATGACACAGATCCTTCTGTAGAGGTATCCTGAGATCAAT 648
Db      |||||
Qy 708 GGAATCAGCAGAATACTATGCTGAGAACAAATATTGCCATGCCAAGACGAGGGG 761
Db      |||||
Qy 649 GGAATCATCTCAATATTATTTCAGAGAATAATATTGATGTGCTCGAGGGTAGTG 702
Db      |||||

RESULT 14
US-10-425-115-112285/c
; Sequence 112285, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 112285
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_33892C.1
US-10-425-115-112285

Query Match          4.9%; Score 108.4; DB 8; Length 466;
Best Local Similarity 57.3%; Pred. No. 7.6e-19;
Matches 196; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 1427 CCGTATATCATATCTATGTCAGAGAAAGGGAGGTTTGAGATGGAGTCCATTACCTGA 1486
Db      |||||
Qy 465 CGGTTTCCCGCTGTTTCCAGAGAAAGGGCGGTTTTAGTCAAGAGACCTTTTATGG 406
Db      |||||
Qy 1487 GGTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTGTTTGAAGTTTCATCCC 1546
Db      |||||

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725 ACTTTTGAATTCACACAGATTCTTCTGTAGAGGTATCTCGGATCAATGGAATCATCT 784

718 GAATACCTATGCTGAGAACAAATATTGCCATGGC 749

785 CAATATTATTCAAAAGAATAGTATTGATGTGCC 816

Search completed: February 19, 2006, 19:02:27

Job time : 2481 secs

405 GATCGGCGCCGTTTACCCCTGGAGCCCTTGGAAATTTTTCAGTCTCGGTAAATTTAGGTCCC 346

1547 TGAATCTTGTGCTGTATGGAAGACTGAAAGGCTGAAGTTATAAGAGGGGGAGTGTCTT 1606

345 CCCACCCGTTCTTCTTGTGAAGGATGAAAGGCCGCCCCAGTATTTAAAGGGGGGGTGGCC 286

1607 TAAACACTCAAAATATATACCAATTTGCTTGACACAGAGCAAGCTCTTTATACCTTCA 1666

285 TGGAACTAAACAGAAATTTTCCCGCTGGGTTTAAACCAACGTCAGGCTTTGTGCGGTTTCA 226

1667 GCTTCAAGGTGATGCTGATTTTTCAGGAGTCACTTGGAGAACAAATCTTGTGCCAAGTTTG 1726

225 GATTTAAGAGATGGTTTGTGACCCCGGCCATACCTCCAGACCCCTCCCTGTGCAAGCTTT 166

1727 AAGTCATTTTGTGTAGCATGCGCTAAATGGTACCTCTGTCTC 1768

165 AAGTTATTTTGTGGAACCTTTGCTTTAGGGTTACGTTTGCCC 124

RESULT 15

US-10-425-115-172748

Sequence 172748, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 172748

LENGTH: 860

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_89129C.1

US-10-425-115-172748

Query Match 3.9%; Score 86.8; DB 8; Length 860;

Best Local Similarity 52.9%; Pred. No. 1.1e-12;

Matches 239; Conservative 0; Mismatches 202; Indels 11; Gaps 2;

309 ATGAGCAATCTAATGCTCTTGTGTTGCCCTTGTGTCATCGCGAGATCGCGTTTCT 368

365 ATGGAGGTGCTTGTGCTCACTCTTGTAGCGTGCCTTCTTGTGAGATCACCTCCCT 424

369 GGGTAGGTGGATATGCGCAAAACCGCCGCTGTTGACTCCCTCGCTGACTTCTTCTA 428

425 TTGCGGCTCGACATGCGAGAGACCGCGAGTGGTCGAGAGCTAGACACAGCTCCTTTTA 484

429 CCGCTC-----TCGAGGGTCTGTTGAAGTGACGATTTGGGTTGGTTGTGGC 479

485 CCACTGCTCTCCCATTTGGGGTGAAGCCGTGGGTGGGGCGTGGTCCCGAGGTGAGCAG 544

480 TTCTGATCGGNATTTCTGAATCGTATAGTTGTGAGGAATGGTTGGAGAGGAGGATGCTGT 539

545 CGATGGCGAGGATGAAGAGATCCGATGGTGGCAGCAGCGGTTTCGAGAGGAGGATGCTGT 604

540 CACGTATTCGAGGGGCTTTTCCAAAGAGCCCTATTTTGTGTTCTCGAGCTGATCAGGAGTG 599

605 GCCCTACGACCGCGACGTTGACAGGATCCCGTGTGTCGCTGGCGCAGCCAAAGGACTG 664

600 GAAGTCGTGTTGCGTTGATGTAATTG--GGTTTAGTGGGATAGAAAGCCAGATGCC 657

665 GAGTAAATGCTACGTAGGTGTTGTAATTTTCTGCGAGTAAGACACTTGTATGCT 724

658 GCATTTGGGTTTACCTCAACCAAGTGAACAGCTAGCAATTCGCGATCAATGGAATCAGCA 717

Result No.	Score	Query			DB	ID	Description
		Match	Length	\$			
C	1	47.4	2.2	1693	12	US-11-136-527-1569	Sequence 1569, Appl
	2	43.6	2.0	1705	12	US-11-128-061-736	Sequence 736, Appl
	3	43.6	2.0	1705	12	US-11-128-049-736	Sequence 736, Appl
	4	41.6	1.9	1141	6	US-09-925-065A-65761	Sequence 65761, A
	5	41.6	1.9	1657	12	US-11-112-908-297	Sequence 297, Appl
	6	41.6	1.9	157230	12	US-11-112-908-64	Sequence 64, Appl
	7	41.6	1.9	170508	12	US-11-112-908-62	Sequence 62, Appl
	8	41.6	1.9	173115	12	US-11-112-908-65	Sequence 65, Appl
C	9	41.4	1.9	577	6	US-09-925-065A-601955	Sequence 601955,
	10	41	1.9	645	6	US-09-925-065A-486277	Sequence 486277,
	11	40.4	1.8	600	6	US-09-925-065A-566981	Sequence 566981,
	12	40.4	1.8	622	6	US-09-925-065A-378838	Sequence 378838,
	13	40.4	1.8	622	6	US-09-925-065A-566980	Sequence 566980,
	14	40	1.8	600	6	US-09-925-065A-325832	Sequence 325832,
	15	39.8	1.8	504	6	US-09-925-065A-355751	Sequence 355751,
	16	39.6	1.8	661	6	US-09-925-065A-222635	Sequence 222635,
C	17	39.4	1.8	584	6	US-09-925-065A-222820	Sequence 222820,
	18	39.2	1.8	424	6	US-09-925-065A-258356	Sequence 258356,
C	19	39.2	1.8	588	6	US-09-925-065A-378836	Sequence 378836,
	20	39.2	1.8	622	6	US-09-925-065A-378836	Sequence 378836,

Query Match 2.2%; Score 47.4; DB 12; Length 1693;
Best Local Similarity 34.7%; Pred. No. 0.41;
Matches 119; Conservative 55; Mismatches 169; Indels 0; Gaps 0;

QY 1852 TGCCTAGTTTCTTGCCCAACTCATTGATCTTTGTATAGACATCACACTTAATTTAA 1911
|::||:| |::| |:|:| | | : | : | : | : | : |

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Db      883  TRVTCGCTTADYGTCTAAVTMAAATTTTTTAAAAACAMGSCCAABGTMGTGTTGTTT 824
Qy      1912  ACTGTTTCGTAGAAGTGAATCCATATTTTAAATGCTTAGTTTATGCTCTTATCTGA 1971
Db      823  GAGATKYTGAAATTAATAGSAAATAYATTTTCAKRAATCATTTAAWGCTTTWTBTYTTG 764
Qy      1972  TCATCTAGAAGTCACAGTCTCTTGATATTTGAGTGAAGAACTGAAATCTAATAGAAGAT 2031
Db      763  YGACAGTTANGCMAATVAGTTGAAATCCATATGTTCCCTGASATATTTTATCMCAAGC 704
Qy      2032  CAGATGTTTCACCAAGACACATATTAATCTCATGTTGTTTATGATGATCTCGAGCTTTT 2091
Db      703  CMCAHGTYGWTATATAAGSCASATVGYMATATATATATAATCCTGAAATCATGAACATGY 644
Qy      2092  TAGTGTCGGAACGTGCTCCCTGTGTTTGAGCAGCTGTTATGCTTCAAGTGTACTGTCCA 2151
Db      643  TCASYSATTTTCCTCCCTGAGTTGAAAHKATKHTATYTGKMCATTTWAAATGGC 584
Qy      2152  GTGCTTATCGTTTGTGACCTCTAAATGAAAAAATGAAAAA 2194
Db      583  AAAATWKGATATYKATTWMSMTMAAAAAAARWMAWVHGAA 541

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RESULT 2

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US-11-128-061-736
; Sequence 736, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Miller, Christopher P.
; APPLICANT: Brown, Eugene L.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 736
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1505)..(1521)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-736

```

```

Query Match      2.0%; Score 43.6; DB 12; Length 1705;
Best Local Similarity 63.2%; Pred. No. 3.3;
Matches 67; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy      1027  AAATTTAGCTTAGCGTTTGAATTCGAATGAGGAAGATTATGTAACCTGAAAAATTTCTTC 1086
Db      776  AAATTTATCTTTCTTTTGAATACTCAATTCACAAAGATTACATCCGGAAGAGCTCTAC 835
Qy      1087  CAATCCCTGTGTGTCGAACCTGTCCTGTGGTTGTTGGTGCTCCAA 1132
Db      836  AATGCATTTTGGCTGCTCAGTACCTGTTCTTCTGGGACCATCCA 881

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RESULT 3

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US-11-128-049-736
; Sequence 736, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 736
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1505)..(1521)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-736

Query Match      2.0%; Score 43.6; DB 12; Length 1705;
Best Local Similarity 63.2%; Pred. No. 3.3;
Matches 67; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy      1027  AAATTTAGCTTAGCGTTTGAATTCGAATGAGGAAGATTATGTAACCTGAAAAATTTCTTC 1086
Db      776  AAATTTATCTTTCTTTTGAATACTCAATTCACAAAGATTACATCCGGAAGAGCTCTAC 835
Qy      1087  CAATCCCTGTGTGTCGAACCTGTCCTGTGGTTGTTGGTGCTCCAA 1132
Db      836  AATGCATTTTGGCTGCTCAGTACCTGTTCTTCTGGGACCATCCA 881

RESULT 4
US-09-925-065A-65761
; Sequence 65761, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65761
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-65761

Query Match      1.9%; Score 41.6; DB 6; Length 1141;
Best Local Similarity 53.8%; Pred. No. 8.3;
Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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RESULT 8

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US-11-112-908-65
; Sequence 65, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 173115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-65

Query Match      1.9%; Score 41.6; DB 12; Length 173115;
Best Local Similarity 53.8%; Pred. No. 69;
Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 1531 TTGAAGTTCACATCCCTGATCTGTGCGCTGATGGAGACTGAAAGCGCTGAAGTTATA 1590
Db 42228 TTGAAGAACACCCGACTGTATCTCATGCTCGGCTGACCAATGAGTAAGCAAAAGTGTTA 42287

Qy 1591 AGAGGGGGAGTGTCTTAAACTCTACAAATATACCCAAATGGCTTGCACACAGACACAA 1650
Db 42288 TGGGGGAGACAGCTTCTAATCTCGACATTTATAAATAATCCACACAGGTACCC 42347

Qy 1651 GCTCTTTATACCTTCAGCTTCAAGGTGAGTGCTGATTTCA 1690
Db 42348 GTGCAATCAATTTTCAGTTCTTAGGATGAGAGATATGTCA 42387

RESULT 9
US-09-925-065A-601955/c
; Sequence 601955, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 601955
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-601955

Query Match      1.9%; Score 41.4; DB 6; Length 577;
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Best Local Similarity 62.4%; Pred. No. 6.9;
Matches 63; Conservative 1; Mismatches 37; Indels 0; Gaps 0;

Qy 10 AAGCGTCATTTTCTTTTCTTTCAGGGAACCATCCACCATAACACAAAAAACAA 69
Db 328 ATCAITGCAGCTTGGTGTGTTTTTTGTAGTAGTACACAAACAATAACAAAAAAA 269

Qy 70 CAGCAAGCTGTGTTTTTTTATCGTTCTTTTCTTTTAAACA 110
Db 268 CAGGCTTTCTGTTCTCTCAATGATGTATTTTCTTCAAAA 228

RESULT 10
US-09-925-065A-486277/c
; Sequence 486277, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 486277
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-486277

Query Match      1.9%; Score 41; DB 6; Length 645;
Best Local Similarity 62.6%; Pred. No. 9.1;
Matches 62; Conservative 1; Mismatches 36; Indels 0; Gaps 0;

Qy 564 AGAGCCTATTTTGTTCGAGCTGATCAGGAGTGAAGTCTGTCGTTGATCTAA 623
Db 217 AGGCGCTCCTTATGTTTCTGAGCTGTCTCTTGTCAATGTTTGTGAGTTTATTA 158

Qy 624 ATTGTGGTTTAGTGGGATAGAAAGCCAGATGCCGCAAT 662
Db 157 GATTAGGATTTGCTGCAATTCAGGGGAATGCGAAT 119

RESULT 11
US-09-925-065A-566981
; Sequence 566981, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
```


Best Local Similarity 45.2%; Pred. No. 16;
Matches 183; Conservative 1; Mismatches 218; Indels 3; Gaps 1;
Qy 1719 CAAGTTTGAAGTCATTTTGTGTAGCATGCGCTAAATGTTACCTCTGCTCTACCTGAATT 1778
Db 21 CAGGTTTGAACACACTCTTTTGTAGAAACTGCAAGGGGATAATTGCACTCTTTGAGGAGT 80
Qy 1779 AGCTTCACCTAGCTGAGCAGTCTAGTAGAGTTTGTAGGAATGAGTATGCGAGTGAATATGGC 1838
Db 81 ACCGTAGTAAGGAAATTAACCTCTATARAAGACAGACAGAGCTTTCTCAGAAAATCT 140
Qy 1839 ATGGCTTTTATTTATGCTAGTTTCTTGGCCAACTCATTTGATGTTTGTATAAGACATCAC 1898
Db 141 TTGGGATGATTGATTGAACTCACAGAGCTGAGCAATTCCTTGGATGTAGCAGTTTAGAA 200
Qy 1899 AC---TTTAATTTTAAACTTTTCTGTAGAAAGTGCAATCCATATTTAATGCTTAGTTT 1955
Db 201 ACACACTTTCTGCAGAAATCTGCAAGTGCATATTTGGACCTCTGTGAGGAATTCGTTGAA 260
Qy 1956 TAGTGCTTATCTGTATCATCTAGAAGTCACAGTCTCTGTATATTTGTGAGTGAATACTGA 2015
Db 261 ACGGGATAATTTTCAGCTGACTAAACAGAGCAGTCTCAGAAATCTCTTTGTGATGTTGC 320
Qy 2016 AATCTAATAGAAGGATCAGATGTTTCACTCAAGACACATTTACTTTCATGTTGTTTGA 2075
Db 321 ATTCAATCCCCAGTTGAACCTTTCCTTTCAGAGTTTCCAGTCTCAGAAATCTCTTTTGA 380
Qy 2076 TGATCTCGAGCTTTTGTAGTGTCTGGAACGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2120
Db 381 GGATCTACAAGTGGATATTTGGACCACTCTGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCT 425

Search completed: February 19, 2006, 18:25:01
Job time : 653 secs

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 566980
LENGTH: 600
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-566980
Query Match 1.8%; Score 40; DB 6; Length 600;
Best Local Similarity 53.0%; Pred. No. 15;
Matches 107; Conservative 1; Mismatches 91; Indels 3; Gaps 1;
Qy 1941 TTTAATGCTTAGTTTGTAGTCTTATCTGATCATCTAGAAGTCACAGTCTTCTGTATATT 2000
Db 85 TTTTGTGACATTTTATGTTTGTAGTTTGTAGTTTGTAGTTTGTAGTTTGTAGTTTGTAGTTT 144
Qy 2001 GTGAGTGAACACTGAATCTAATAGAAGGATCAGATGTTTCACTCAAGACACATTTATAC 2060
Db 145 CTTAGGAAACAAAGTCTTTTATTATATGATAA---TTTCTGTGATTTGCTTTCTACT 201
Qy 2061 TTCATGTTGTTTGTATGATCTCGAGCTTTTGTAGTGTGAACTGCTGCTGCTGCTGCTGCTG 2120
Db 202 TCTGTGATGTTTGTACCAAGCACAAATTTTAAATTTTGTAGTGTCTAAATTAATCTATTT 261
Qy 2121 GCACCTGTTATTGCTTCAGTGT 2142
Db 262 TCWTTTGTGTTGTGCTTTT 283

RESULT 15
US-09-925-065A-325832
Sequence 325832, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 325832
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-325832

Query Match 1.8%; Score 39.8; DB 6; Length 504;

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2006, 15:41:43 ; Search time 8807 Seconds
(without alignment)
11676.849 Million cell updates/sec

Title: US-09-913-858c-1
Perfect score: 2198
Sequence: 1 actaactcaaacgtgcatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hcc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	533	24.2	861	8	CX710861 gmrtDrNS0
2	512.6	23.3	806	7	CO076716 GR_Ea38C
3	489.6	22.3	584	7	CV537942 NOD_248 D
c 4	462	21.0	782	8	CX710693 gmrtDrNS0
5	457.6	20.8	800	7	CX120486 218109.p1
6	447.6	20.4	863	6	CB669685 OSUNE02F
7	437.6	19.9	532	3	BM143091 saj39d07.
8	430.4	19.6	862	8	DN798206 USDA-FP/A
c 9	422.8	19.2	865	6	CB656872 OSUNE01L
10	414.4	18.9	744	6	CD813251 BN15_019A
11	401.4	18.3	818	7	CO072619 GR_Ea310
12	394.8	18.0	665	6	CD813104 BN15_001I
13	378.6	17.2	689	3	BM099511 EBes01_SQ
14	375.4	17.1	641	6	CF770670 DSBF1_9 C
15	371	16.9	599	7	CV534954 NOD_210 G
16	369.6	16.8	651	5	BQ592743
c 17	364.4	16.6	422	6	CA800844 sat25f03.
18	354.2	16.1	539	1	AU292612 AU292612
19	341	15.5	551	3	CA008944 HUI2K09r
20	337.2	15.3	571	3	BJ464838 BJ464838
21	332.2	15.1	517	2	BG790911 sae71e02.
22	331.8	15.1	588	6	CF303361 ABF1--02-

23	326.2	14.8	811	6	CB656871	CB656871 OSUNE01L
c 24	326	14.8	675	8	DR930577	DR930577 EST112211
25	321.2	14.6	683	6	CA197183	CA197183 SCRPAD102
26	320.4	14.6	651	7	CN190564	CN190564 UCRCS06_0
27	317	14.4	842	7	CN818044	CN818044 HRO4472-D
28	313.2	14.2	753	6	CB646605	CB646605 OSUNE09C
29	292.4	13.3	700	8	DN157236	DN157236 GCN002H22
c 30	288.4	13.1	685	8	DN187833	DN187833 HO24L21w
31	284	12.9	729	6	CF770757	CF770757 DSBF1_9 C
c 32	280.2	12.7	690	5	BQ659171	BQ659171 HD01K23w
33	277.8	12.6	559	6	CA276866	CA276866 SCRLSD201
c 34	276	12.6	722	8	DR814720	DR814720 ZM_BPB004
35	271.2	12.3	560	7	CK066728	CK066728 73336r81c
36	269.6	12.3	793	8	DR174909	DR174909 HR0004_12
37	268	12.2	598	7	CK008937	CK008937 28456r81c
c 38	262	11.9	911	10	CG142421	CG142421 PUFUG43TB
c 39	257.8	11.7	701	3	BQ167130	BQ167130 WHE0945 F
40	257.6	11.7	786	8	DN908926	DN908926 57449.2 D
41	256	11.6	606	7	CK764534	CK764534 aam01-7ms
c 42	255.4	11.6	679	7	CO072618	CO072618 GR_Ea310
43	255	11.6	831	6	CF446084	CF446084 EST682429
44	254.2	11.6	395	6	CF349923	CF349923 fc3174_e
45	252.8	11.5	832	8	DR818536	DR818536 ZM_BPB005

ALIGNMENTS

RESULT 1
CX710861/c
LOCUS CX710861 861 bp mRNA linear EST 21-JAN-2005
DEFINITION gmrtDrNS01 24-D M13R C08 060.s4 Water stressed 48h segment 2
gmrtdrNS01-Glycine max cDNA 3', mRNA sequence.
ACCESSION CX710861
VERSION CX710861.1 GI:58024120
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

REFERENCE 1 (bases 1 to 861)
Valliyodan,B., Huang,S., Joshi,T., Hernandez,A., Spollen,W.G., Bohnert,H.J., Duke,M.V., Liu,X., Scheffler,B.E., Sharp,R.E., Xu,D., Springer,G.K., Stacey,G. and Nguyen,H.T.
EST Analysis of Soybean Root Tip Under Drought Stress: MSNC Grant 00245 - Development and Deployment of Biotechnology Tools for Soybean Improvement
Unpublished (2005)
Contact: Henry T. Nguyen
Molecular Genetics and Biotechnology
University of Missouri-Columbia
National Center for Soybean Biotechnology, 1-87 Agriculture Bldg., MO 65211, USA
Tel.: (573)882-5494
Fax: (573)882-1469
Email: nguyenhenry@missouri.edu
POLYA=Yes.

JOURNAL
COMMENT

FEATURES
source

Location/Qualifiers
1..861
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams82"
/db_xref="taxon:3847"
/dev_stage="Droughted Roots"
/clone_lib="gmrtDrNS01"
/note="Vector: pBS II SK(+); Funding: The production of EST's submitted in this project was funded by MSNC Grant 00245 - Development and deployment of biotechnology tools for soybean improvement, to H.T. Nguyen as Principal Investigator. Sample collection and library construction: Dark grown soybean seedlings with primary roots were

transplanted to high (-0.05MPa) or low water potential (-1.6MPa) vermiculite, and harvested at 5h and 48h after transplanting. Each root tip was divided into two segments (distances are from the junction of root apex and root cap): segment 1, 0-3mm; and segment 2, 3-11mm. Total RNA was extracted by the 'hot phenol' method (Plant Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)⁺mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)⁺mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. The double stranded cDNAs were size-selected (>500 bp). Size selected cDNAs were adapted with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The gmtDrNS01 library was created by subtracting the well-watered soybean root library from the water-stressed (5h and 48h) soybean root libraries. The double stranded plasmid DNA from the primary library was converted to single-stranded circles and used as a template for PCR amplification. The purified PCR products, representing the entire cDNA population cloned were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B E. coli. Clone requests: Requests for clones should be made to Dr. Henry Nguyen, National Center for Soybean Biotechnology, 1-87 Agriculture Bldg., University of Missouri-Columbia, MO, 65211. Email: nguyenhenny@missouri.edu
TAG TISSUE=Water stressed 48h segment 2
TAG_SEQ=TCGGA"

ORIGIN

Query Match 24.2%; Score 533; DB 8; Length 861;
Best Local Similarity 84.5%; Pred. No. 2.2e-129;
Matches 662; Conservative 0; Mismatches 105; Indels 16; Gaps 5;

1223 TAGCAGAAAATCCGAGCATATATCAATCATGAGTGGAGTATGAGGCTCCATCTG 1282
861 TAGCAGAAAATCCTGAGCATATATCATCTTTGAGTGGAGTATGAGGCTCCATCTG 802

1283 ACTCCTTCAAGGCCCTTGTGATATGGCAGCTGTGCATTCATCGTCCGCTTTGCATTC 1342
801 ATTCCTTCAAGGCCCTTGTGATATGGCAGCTGTGCATTCATTCCTCGCGCTTTGCATTC 742

1343 ACTTGGCCACAGTGAAGT 1402
741 ACTTGGCCACAGTGAAGT 682

1403 GCAGTGCATAGT 1462
681 GCAGTGCATAGT 622

1463 TTGAGATGAGTCCATTTACCTGAGGCTAGCAATTTAACTCTCTGAATGCTGTGAAGCTG 1522
621 TTGAGATGAGTCCATTTACTTGAAGTCTAGCAATTTAACTCTTGAAGCTTGAAGTTG 562

1523 CTGTTGTTGAAGTTACATCCCTGATCTGTGCTGATGAGAGCTGAGAGAGAGAGT 1582
561 CTGTTGTTTCAAGTTACATCCCTGATCTGTGCTGATGAGAGAGAGAGAGAGT 502

1583 AAGTTTAAAGT 1642
501 AAATTTCTTAGT 442

1643 AGAGACAAGCTCTTTATACCTTCAAGCTTCAAGGTGATGCTGATTTCAAGAGTCACTTGG 1702

441 AAAGCAAGCTCTTTATACCTTACGTTCAAGGGGATGCAGATTTTCAAGAGTCACTTGG 382
1703 AGAACAATCCTTGTGCCAAGTTTGAAGTCATTTTGTGTAGCATCGCTAATGCTACCT 1762
381 AAAGCCATCTTGTGCAAAAGTTTGAAGTCATTTTGTGTAGCATGTGCT-AGTGGCCTCT 323
1763 CTGCTCTACCTGGAAT--TAGCTTCACTTAGCTGAGCACTAGCTAGAGTTTGTAGGAATGAG 1820
322 CTGCTCTACATGAATAGCTTCTTCACTTAACCTGAGC-----GGTAGAGTTTGGGATGAG 267
1821 TATGCACTGAATATGCGCATGCTTTATTTATGCTAGTCTTTCTGGCCAACTCATGTATG 1880
266 TATGCACTGAATATGCGCATGCTTTATTTATGCTAGTCTTTCTGGCCAACTCATGTATG 207
1881 TTTTCTATAAGACATCACACTTTAATTTTAACTTGTCTGT---AGAGTGCAATCC 1937
206 ATTTATATTCAAAAGATAATCTTACTTTTGAACCTCTTTTGTGTACAAGAGGTGAGGTTCC 147
1938 ATATTTATGCTTACTTTTAGT-----GCTCTTATCTGATCATCTAGAAAGTCAAGTTTC 1991
146 ATATTTAATGCTTACTTTTAGTTTTAGTATAGAGTTTCTATCTGATCATCTAGAAAAGCCACATG 87
1992 TTG 1994
86 ATG 84

RESULT 2

CO076716 806 bp mRNA linear EST 15-JUN-2004
LOCUS GR_Ea38C24.r GR_Ea Gossypium raimondii cDNA clone GR_Ea38C24 3',
DEFINITION mRNA sequence.
ACCESSION CO076716
VERSION CO076716.1 GI:48746197
KEYWORDS EST.
SOURCE Gossypium raimondii
ORGANISM Gossypium raimondii

REFERENCE 1 (bases 1 to 806)
AUTHORS Kim H., Yu Y., Kudrna, D., Hatfield, J., Stum D., Mueller, C., Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and Wing, R.A.

TITLE Global assembly of Cotton ESTs
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 38 row: C column: 24.

FEATURES

source 1.806
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Ea38C24"
/tissue_type="whole seedlings"
/dev_stage="first true leaves"
/lab_host="DH10B"
/clone_lib="GR_Ea"
/notes="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."

ORIGIN

Query Match 23.3%; Score 512.6; DB 7; Length 806;
Best Local Similarity 78.2%; Pred. No. 5.4e-124;
Matches 628; Conservative 0; Mismatches 174; Indels 1; Gaps 1;

gmtrDrNS01 library was created by subtracting the well-watered soybean root library from the water-stressed (5h and 48h) soybean root libraries. The double stranded plasmid DNA from the primary library was converted to single-stranded circles and used as a template for PCR amplification. The purified PCR products, representing the entire cDNA population cloned were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B E. coli. Clone requests: Requests for clones should be made to Dr. Henry Nguyen, National Center for Soybean Biotechnology, 1-87 Agriculture Bldg., University of Missouri-Columbia, MO, 65211. Email: nguyenhenny@missouri.edu TAG_TISSUE=Water stressed 48h segment 2 TAG_SEQ=TCGGA"

ORIGIN

Query Match 21.0%; Score 462; DB 8; Length 782;
Best Local Similarity 83.5%; Pred. No. 1.3e-110;
Matches 588; Conservative 0; Mismatches 100; Indels 16; Gaps 5;

QY 1302 GGATATGCGAGCTGTGCATTTCATCGTCGCTCTTTGCAATTCACCTTGGCCACAGTGAGTAG 1361
DB 782 GGATATGCGAGCTGTGCATTTCATCGTCGCTCTTTGCAATTCACCTTGGCCACAGTGAGTAG 723
QY 1362 ACAGAAAGGAGAAAATAATCCAAAGCCTTTAAAGAGACGTCTTCCAAAGTGACCTAGAGGGCC 1421
DB 722 AGAGAAAGGAGAAAATAATAGTCCAGGCTTTAAAGAAACGCCCTTCCAAAGTGAGTAGAGGGCC 663
QY 1422 AGAAACCGTATATCATATCTATGTGAGAGAAAGGGAGGTTTGAGATGAGTCCCAATTTA 1481
DB 662 AAAAAGCTGTATCATATATTTATGTGAGAGAAAGGAGGTTTGAGATGAGTCCCAATTTA 603
QY 1482 CCTGAGGTTACCAATTTAACTCTGAATGCTGAGAGGCTGCTGTTGTTGTTGTTGAGTTTCA 1541
DB 602 CTTGAGGTTAGCAATTTAAACCCCTTGAGGCTTGAAGTTGCTGTTGTTGTTGTTGTTGTTCA 543
QY 1542 ATCCCTGTAATCTTGTGCTGTATGGAAGACTGAAGGCTGAAGTTTATAGAGGGGGGAG 1601
DB 542 ATCCCTGTAATCATGTATACCTATATGGAAGACAGAAAGACCTGAAATTTCTTAGAGGGGGCAA 483
QY 1602 TGCTTTAAAGCTTCAAAAATATACCCAAATGGCTTGACACAGACAGCAAGCTCTTTATATAC 1661
DB 482 TGATTTAAAGCTTCAAAAATATATACCCAGTTGGGTTGACACAAAGACAAAGCTCTTTATAC 423
QY 1662 CTTGAGGTTCAAGGGTGATGCTGATTTTCAGGAGTCACTTGGAGAAACAATCTTTGTGCCAA 1721
DB 422 CTTGAGGTTCAAGGGTGATGAGATTTTCAAGAGTCACTTGGAGAAAGCAATCTTTGTGCCAA 363
QY 1722 GTTTGAAGTCAATTTTGTGTAGCATGCGCTAAATGGTACCTCTGCTCTCTCTCTCTCTCTCTCT 1779
DB 362 GTTTGAAGTCAATTTTGTGTAGCATGCTGCT-AGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCT 304
QY 1780 GCTTCACTTGTAGCAGCACTAGTAGTTTGTAGGATGATGAGTGGCAGTGAATATGSCA 1839
DB 303 TCTTCACTTAACTGAGC---GGTAGAGTTTGTAGGATGATGAGTGGCAATGAAACTGGCA 248
QY 1840 TGGCTTTATTTATGCGCTAGTTTCTTGGCCAACTCATTGATGTTTGTGTATAGACATCACA 1899
DB 247 TGGCTTTATTTATGATAGCTTCTTGGCCAACTCATTGATGATGATGATGATGATGATGATGATG 188
QY 1900 CTTTAAATTTTAAACTTCTTTTCTGT----AGAGTGCAAAATCAATATTTAAATGCTTAGTTT 1956
DB 187 TCTTACTTTTGAACCTCTTTTGTGTAGCATGCTGCT-AGTGGGCTCTCTCTCTCTCTCTCTCTCT 128
QY 1957 AGT-----GCTCTTATCTGATCATCTAGAGTCAAGTCAAGTCTTG 1994
DB 127 AGTTATAGAGTTTCTCTCTGATCATCTAGAAAGCCACATGATG 84

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RESULT 5
CK120486      800 bp      mRNA      linear      EST 01-JUN-2004
LOCUS
DEFINITION    218i09.pl AtM1 Arabidopsis thaliana cDNA clone MPMGp2011109218
5-PRIME, mRNA sequence.
ACCESSION
VERSION       CK120486
KEYWORDS
SOURCE
ORGANISM      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 800)
Feilner T., Immink R.G.H., Cahill D.J. and Kersten B.
Generation of a cDNA expression library from Arabidopsis
inflorescence meristem
Unpublished (2003)
CONTACT      Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Innestr. 73, D-14195 Berlin, Germany
Tel.: +49(0)30/84131648
Fax: +49(0)30/84131128
Email: Kersten@molgen.mpg.de
Insert Length: 800 Std Error: 0.00
Plate: 218 row: 1 column: 9
Seq primer: pQE65.
FEATURES
Location/Qualifiers
1..800
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="GABI:955906"
/db_xref="taxon:3702"
/clone="MPMGp2011109218"
/tissue_type="inflorescence meristem"
/dev_stage="about one week after bolting"
/lab_host="E. coli SCS-1/pSE111"
/clone_lib="AtM1"
/notes="vector: pQE-3ONAST-attB (AY386205); Site 1: SalI;
Site 2: NotI; About 1 week after bolting, cDNA synthesis
using SuperscriptTM-system (Invitrogen) with an
oligo(dT)-primer containing NotI restriction site and a
SalI adapter. The main library (plate numbers begin with
1) of 38,000 clones was rearrayed into the sublibrary
(plate numbers begin with 201) containing 5,000 putative
expression clones. Average insert size is 1 kb. Note: The
rearrayed sublibrary (plate numbers begin with 201) was
sequenced. Library generation and sequencing was granted
in context of GABI-LAPP; data are also accessible at
https://gabi.rzpd.de"
ORIGIN
Query Match      20.8%; Score 457.6; DB 7; Length 800;
Best Local Similarity 73.8%; Pred. No. 2e-109;
Matches 580; Conservative 0; Mismatches 206; Indels 0; Gaps 0;
Qy 633 TAGTGGGGATAGAAAGCAGATGCCGATTTGGTTTACCTCAACCAAGTGGACAGCTAG 692
Db 5 TAGTTCAGGGAAACACACAGATGCTGGTTGGATTAGGTCAGAAACCTGGAACTCTTAG 64
Qy 693 CATTCCTGGATCAATGCAATCAGCAATATCTAGTCTGAGACAAATATGCCATGGCAAG 752
Db 65 TATAATACGTTCCATGGAATCAGACACAGTATATCCAGAAATATCTTGACAGGGCAGC 124
Qy 753 ACGGAGGGGATATAACATCGTAATGCAACACAGCTATCTTCGGATGTTCTCTGTTGGATA 812
Db 125 ACGGAGAGGTTATGATATAGTAGTATGACACACTAGTCTATCATCAGATGTTCTGTTGGATA 184
Qy 813 TTTTTCATGGGCTGAGTATGATATGATGGCCAGCAGCCGAGAAACTGAAGCTGCTCT 872
Db 185 TTTTTCGTCGGCGAGTATGATATATATGTTCTCCGGTACAGCCAAAACTGAGAGAGCTAT 244

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Qy 873 TGCAGCTGCTTTTCATTTCCAAATTTGGTGTCTCGAAATTTCCGGTTGCAAGCTCTTGAGGC 932
Db 245 TGCAGCTGCTTTTCATTTCCAAATTTGGTGTCTCGAAATTTTCGTTCTACAGCACTTGAGGC 304
Qy 933 CTTTGAATAATCAAAATCAAAATGATTTCTTATGGTGGTTGTGCACAGGAACCGTATGG 992
Db 305 ATTGATCAAAACTAAACATTAAGATTGATTTCTTATGGTGGTTGTGCATCGAAACCGGATGG 364
Qy 993 AAGAGTGAACAAAGTGGAGCCCTGAGGACTACAAATTTAGCTTAGCGTTTGAATAATTC 1052
Db 365 GAAAGTTGACAAAGTTGAAGCTCTTAAGCGATACAAATTCAGTTTGGCTTTTGAGAATAC 424
Qy 1053 GAATGAGGAAGATTATGTAACTCAAAATTTCTTCCAAATCCCTTGTTCCTCGAACTGTCCC 1112
Db 425 TAACGAGGAGATTAATGTACCCAGAGATTCTTTCAATCCTTAGTTGCTGGTCCGTTCCC 484
Qy 1113 TGTGGTTGTTGGTCTCCAAATATTCAGGACTTTGCTCTCTCTCGTGGTTCAATTTTACA 1172
Db 485 CGTGGTAGTTGGTCTCCAAATATAGAAGAAATTTGCGCTTGTCTCGGACTCATTCCTTCA 544
Qy 1173 TATTAAGAGATAGAGATGTTGAGTCTGTTGCAAGAGACCATGAGATATCTAGCAGAAA 1232
Db 545 CATTAAGACTATGGAAGATGTAGGCCAGTTGCAAGAGAGAAATGAAGTATCTCGACGTAA 604
Qy 1233 TCCCGAAGCATATAATCAATCATTTGAGGTGGAAGTATGAGGGTCCATCTGACTCTCTTCAA 1292
Db 605 CCTGCTGCTTATATCAGACACTAAGATGGAATACGAGGGTCTTTCAGATCTCTTCAA 664
Qy 1293 GGCCCTTGTGGATATGGCAGCTGTGATTCATCGTGGCCGCTTTTGTGANTTACATTGGCCAC 1352
Db 665 GGCACCTGTTGATATGGTCTGTACACTCTTCTTGGCGTCTCTGCAATTTTCTCGGCCAC 724
Qy 1353 AGTGAGTAGAGAGAGAGAAATATCAAGCCCTTAAGAGAGCTCTTGCAGTGCAC 1412
Db 725 GAGGGTCCGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 784
Qy 1413 TAGAGG 1418
Db 785 CAGGGG 790

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RESULT 6
CB669685      863 bp      mRNA      linear      EST 09-APR-2003
LOCUS
DEFINITION    OSJN2E02F21.f OSJN2E Oryza sativa (japonica cultivar-group) cDNA
clone OSJN2E02F21 5', mRNA sequence.
ACCESSION
VERSION       CB669685
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 863)
Jantaseuriyarat C., Gowda M., Haller K., Hatfield J., Lu G.,
Stahlberg E., Zhou B., Li H., Kim H., Yu Y., Dean R.A., Wing R.A.,
Soderlund C. and Wang G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
PUBMED
1588683
COMMENT
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc

```

BACKWARD: gga aac agc tat gac cat g
Plate: 02 row: F column: 21
Seq primer: gta aaa cga cgg cca gtg.

FEATURES

source

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1. 863
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNE02F21"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNE"
/notes="Vector: pBluescript II KS +; Site 1: EcoRI
XhoI; 24 hrs after inoculation with Rice Blast (
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ORIGIN

Query Match	20.4%;	Score 447.6;	DB 6;	Length 863;
Best Local Similarity	70.9%;	Pred. No. 8.8e-107;		
Matches 594;	Conservative 0;	Mismatches 244;	Indels 0;	Gaps 0;
907	Y			
2	b			
967	Y			
62	b			
1027	Y			
122	b			
1087	Y			
182	b			
1147	Y			
242	b			
1207	Y			
302	b			
1267	Y			
362	Db			
1327	Y			
422	Db			
1387	Y			
482	Db			
1447	Y			
542	Db			
1507	Y			
602	Db			
1567	Y			
662	Db			
1627	Y			
722	Db			

Qy	1687	782	839
Db	TTCAGGAGTCACCTTGGAGACAACTCCTTGTGCCAAGTTGAAGTCATTTTGTGAGC	CTTGACAAATACATTAAGATCATCCATGTGCNAAGCTTGAAGTCATTTTGTATAAC	

RESULT 7	
BMI143091	
LOCUS	BMI143091 linear EST 16-JUL-2004
DEFINITION	sa-j3dof.y1 Gm-cl086 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-cl066-5150 5' similar to TR:Q9ST51 FUCT C3 PROTEIN. ; , mRNA sequence.
ACCESSION	BMI143091
VERSION	BMI143091.1 GI:17153158
KEYWORDS	EST.
SOURCE	Glycine max (soybean)
ORGANISM	Glycine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

ORIGIN

Query Match 19.9%; Score 437.6; DB 3;
Best Local Similarity 88.9%;
Pred. No. 3.5e-104; Length 532;


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Db      432  ATGGAATCGGCTTCGTAATTCAGAGAAATAATCTTTGCCAGCAGCAGGAGGGTTAC 491
Qy      766  AACATCGTAATGACAAACCACTGATCTATCTTCGGATGTTCCCTGTTGGATATTTTTCATGGGCT 825
Db      492  GATATTTGTAATGACAACTAGCCTTTCATCGGATGTTCCCTGTTGGATATTTTTCATGGGCC 551
Qy      826  GAGTATGATATGATGACACAGTCAGCGGAAACCTGAAAGCTGCTCTTCAGCTGCTTTC 885
Db      552  GAGTATGATATCATGACACAGTCAGTCAGGAAAGCTGAGAAAGCTGTCAGCTGCTTTC 611
Qy      886  ATTTCCAAATTTGCTGCTCGAAATTTCCGTTTCGAGCTCTTCAGGCTTCGAAATCA 945
Db      612  ATTTCTAAATTTGCTGCTCGGCAACTTTCGTTTTCGAAAGCTTTCGAGCTTTCGAAAGGCA 671
Qy      946  AACATCAAAATTCATTTCTATGCTGTTGTCACAGAAACCGTGATGGAAGAGTGAACAAA 1005
Db      672  AATATCAAGATAGATTTCTATGTTAGTTGCTATGATGCAATCAACGATGGAACGTTGACAAA 731
Qy      1006  GTGGAAGCCCTGAAGCACTACAAATTTAGCTTAGC-GTTTGAATAATTCGAATCAGGAAGA 1064
Db      732  GTTGAACCTGTAAGACGCTATAAGTTTAGCTTGGCTTTTGTAGAACTCCCAATCAGGAGGA 791
Qy      1065  TTATGTAACCTGAAAATTTCTTCCATC 1091
Db      792  TTATGTCACCTGAAAAGTTTCTCCAGTC 818

RESULT 12
CD813104
LOCUS   CD813104
DEFINITION   BN15.00119F011204 BN15 Brassica napus cDNA clone BN15001119, mRNA
sequence.
ACCESSION   CD813104
VERSION     CD813104.1 GI:32495044
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
ORGANISM    Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 665)
AUTHORS    Genoplante.
TITLES     Genoplante, a major partnership french program in plant genomics
JOURNAL    Unpublished (2003)
COMMENT    Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).

FEATURES             source
            1..665
            /organism="Brassica napus"
            /mol_type="mRNA"
            /cultivar="Jet Neuf"
            /db_xref="taxon:3708"
            /clone="BN15001119"
            /cissue_type="seed"
            /clone_lib="BN15"

ORIGIN
Query Match      18.0%; Score 394.8; DB 6; Length 665;
Best Local Similarity 75.8%; Pred. No. 7.8e-93;
Matches 502; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

Qy      799  GTTCTGTTGGATATTTTTCATGGCTGAGTATGATATGATGGCACCAGTCAGCCGAAA 858
Db      1    GTTCTGTTGGATATTTTTCATGGCTGAGTATGATATGATGGCTCGGTTTCAGCCCAAG 60
Qy      859  ACTGAGCTGCTCTGAGCTGCTTCATTTCCAAATTTGCTGCTCGAAATTTCCGGTTG 918

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Db      61  ACCGAGAAGGCTATAGCTGCTCTTTTATTTTCCAACTGTGGTGCTCCGAATTTTCGACTG 120
Qy      919  CAAGCTCTTGGAGCCCTTGAAATAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCA 978
Db      121  AAAGCAGCTTGAAGCCCTGATGAAGAGTAGCATCAAGATTTGATTTATATGTTGGTGTGCAT 180
Qy      979  AGGAACCGTGATGGAAGAGTAGTGAACAAAGTGAAGCCCTGGAAGCCTTACAAATTTTACCTTA 1038
Db      181  AGGAACCGTGATGGAAGAGTAGTGAACAAAGTGAAGCCCTTGAAGCTTCTTGAAGCTTGAAGCTT 240
Qy      1039  GCGTTTGAATAATTCGAATGAGGAAGATTTATGTAACATGGAATAATTTCTTCAATCCCTTTGT 1098
Db      241  GCTTTTGAGAACTAATCAAGGAGGATTTATGTCACCTGAGAGCTTCTTCCAGTCTCTAGTT 300
Qy      1099  GTGGAACCTGCTCCCTGTTGGTGTCTCCAAATATTCAGGACTTTTGTCTCTCTCTCT 1158
Db      301  GCTGGATCTGTACCTGTTGGTGTCTCCGAATATAGATGAATTTTCGCCAGCTTCA 360
Qy      1159  GCTTCAATTTTACATATTAAGAGATAGAGGATGTTGAGTCTGTTGCAAGAGCAGCATGAGA 1218
Db      361  GATTCATTCCTTTACATTAAGAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAG 420
Qy      1219  TATCTAGCAGAAATCCCGAAGCATATATCAATCAATTCAGGCTGGAAGATGAGGCTTCA 1278
Db      421  TATCTGCTGCTTAACTCTGCTTATATCAAGCATTAAGATGGAAGATGGAAGATGGAAGATGGAAG 480
Qy      1279  TCTGACTCTTCAAGCCCTTGTGGATATGGAAGCTGTCAGCTGTCATCTGTCCTCTCTTTC 1338
Db      481  TCAGATCTTCTTCAAGCACTTGTGACATGGCTGCTGTCATCTTCTCTCTCTCTCTCTCTCT 540
Qy      1339  ATTCATCTGCGCACAGTAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1398
Db      541  ATTTCTCTGACCAAGGATCCAAAGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy      1399  CCTTGCAAGTGCACTA---GAGGGCCAGAAACCGTATATCATATCATATCTATGTCAGAGAAAG 1455
Db      601  CCTTGCAAGTGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy      1456  GG 1457
Db      661  GG 662

RESULT 13
BM099511
LOCUS   BM099511
DEFINITION   EBes01_SQ003_H09_R embryo sac, 4-6 DPA, no treatment, cv Optic, EBes01 Hordeum vulgare subsp. vulgare cDNA clone EBes01_SQ003_H09 5', mRNA sequence.
ACCESSION   BM099511
VERSION     BM099511.2 GI:21939242
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
ORGANISM    Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 689)
AUTHORS    Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
TITLES     Development of Barley Transcriptome Resources
JOURNAL    Unpublished (2001)
COMMENT    On Nov 21, 2001 this sequence version replaced gi:17030575.
            Contact: Waugh R, Marshall DF
            Genome Dynamics/Computational Biology
            Scottish Crop Research Institute
            Invergowrie, Dundee, DD2 5DA, Scotland, UK
            Tel: 00 44 1382 562731
            Fax: 00 44 1382 562426
            Email: est@scri.sari.ac.uk
            All sequence has a Phred quality score of 20 or over
            Seq primer: M13 reverse.
            Location/Qualifiers

FEATURES

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source	1. 689	/organism="Hordeum vulgare subsp. vulgare"
		/mol_type="mRNA"
		/cultivar="Optic"
		/sub_species="vulgare"
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		/clone="EBes01 SQ003 H09"
		/tissue_type="embryo sac"
		/dev_stage="4-6 DPA"
		/lab_host="DH10B"
		/clone_lib="embryo sac, 4-6 DPA, no treatment, cv Optic, EBes01"
		/note="vector: pSPORT1; Site 1: Sal I; Site 2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from embryo sacs dissected from developing grains (4-6 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
ORIGIN		
Query Match	17.2%;	Score 378.6; DB 3; Length 689;
Best Local Similarity	71.8%;	Pred. No. 1.5e-88;
Matches	495; Conservative	0; Mismatches 194; Indels 0; Gaps 0;
Qy	877	GCTGCTTCATTCCTCAATTTGCTGCTCGAATTTCCGGTTGCAAGCTCTTGAGGCCCTT 936
Db	1	GCAGCCCTTATTTCCAACTGGCGTGCAGAACTTCCGTTTGCAGCCCTTGAGATGCTT 60
Qy	937	GAAGAAATCAACATCAAAATTTGATTTATGTTGTTGTTGTCTACAGAACCGTGATGGAAGA 996
Db	61	GAAAGCTTAGATGTAAATTTGATTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 120
Qy	997	GTGAACAAAGTGAAGCCCTGAAGCACTACAAAATTTAGCTTAGCGTTTGAAAAATTCGAAT 1056
Db	121	GTGGACAAAGTGGAGACTCTAAAGGGCTACAAATTCAGCTTGGCTTTTGAGAAATTTCTAAT 180
Qy	1057	GAGGAAGATATGTAACTGAAATTTCTTCCAACTCCCTTTGTTGTTGTTGTTGTTGTTGTTGTT 1116
Db	181	GAGGAAGATATGTAACTGAAATTTCTTCCAACTCCCTTTGTTGTTGTTGTTGTTGTTGTTGTT 240
Qy	1117	GTGTT 1176
Db	241	GTGTT 300
Qy	1177	AAAGATAGAGATGTTGAGTCTGTTGCAAGACCATGAGATATCTAGCAGAAATCCCT 1236
Db	301	AAGGAGCTTGATGATGTCATTTCACTTGCAGAGCAATGAAACATATTTGCATCAATCCT 360
Qy	1237	GAAGCATATATCAATCATTCAGGTGGAAGTATGAGGTCCATCTGCTCTTCAAGGCC 1296
Db	361	GATGCTTTTAACTCAATTTGAGGTGGAAGTATGATGTTGTCATCTGATTTCTTCAAGGCA 420
Qy	1297	CTTGTGGATATGGCAGCTGTGCATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1356
Db	421	CTTATTTGATGCGGAGCGGTTTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy	1357	AGTAG 1416
Db	481	ATTCATGAAAG 540
Qy	1417	GGGCCAGAGAAACCGTATATCATATCTATGTCAGAGAAAGGGAGGTTTGAGATGAGATGCC 1476
Db	541	AAAAGAGGAGACAGTATACCACTTATTTGTGAGAGAGAGAGGCGGTTTAAAGACAGAGAAC 600
Qy	1477	ATTTACCTGAGGCTTAGCAATTTAACTCTGTAATGCTGTGAAGGCTGCTGTTGTTTGAAG 1536
Db	601	ATTTATCTAAGATCAGATCAGTTAACTTTAGGAGCTTTGAAGCTTCTGCTGTGCACATATAA 660
Qy	1537	TTACATCCCTGAAATCTTTGTCCTGTATG 1565
Db	661	TTTAGCTCCCTCAAGCATGTTTCTTATATG 689

RESULT 14

CF770670

LOCUS

DEFINITION

DSBF1_9 C11.b1.A010 Drought-stressed before flowering Sorghum bicolor cDNA clone DSBF1_9 C11.A010 5', mRNA sequence.

CF770670

VERSION

CF770670.1 GI:37755274

KEYWORDS

EST.

SOURCE

Sorghum bicolor (sorghum)

ORGANISM

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

1 (bases 1 to 641)

AUTHORS

Cordonnier-Pratt, M.-M., Zhang, D., McCartor, K., Nguyen, H.T. and Pratt, L.H.

TITLE

An EST Database from Sorghum: Subtracted pre-flowering drought stressed leaf tissues

JOURNAL

Unpublished (2003)

COMMENT

Other ESTs: DSBF1_9 C11.g1.A010

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Library constructed at Texas Tech University by Deshui Zhang in the laboratory of Dr. Henry Nguyen. Sequencing was done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAAACAGCTATGACC).

Location/Qualifiers

1. 641

/organism="Sorghum bicolor"

/mol_type="mRNA"

/cultivar="Tx7000"

/db_xref="taxon:4558"

/clone="DSBF1_9 C11.A010"

/dev_stage="Pre-flowering"

/lab_host="ElectroMax DH10B (BRL)"

/clone_lib="Drought-stressed before flowering"

/note="Organ: Leaf; Vector: pBlueScriptSK-; Site 1: XhoI; Site 2: EcoRI; The library was prepared from polyA+ RNA from leaves harvested from pre-flowering, drought-stressed Sorghum bicolor, cv. TX7000. Double-stranded cDNA was cloned unidirectionally using the Unizap system from Stratagene. After amplification, the library was subtracted by re-association hybridization. Inserts can be excised with XhoI and EcoRI."

ORIGIN

Query Match

Best Local Similarity

Matches

475; Conservative

0; Mismatches 166; Indels 0; Gaps 0;

Qy

803

CTGTGGATATTTTCATGCGCTGAGTATGATATGATGCGCACCTGCGTCTCCAAAGACTG 862

Db

1

CAGTTGGCTACTTTTCATGGCTGAATATGATATCATGCGCACCTGCGTCTCCAAAGACTG 60

Qy

863

AAGCTGCTCTTGAGCTGCTTTTCATTCCTCAATTTGGTGGCTCGAAATTTCCGGTTGCAAG 922

Db

61

AAGAAGCTCTTGCTGCGACCTTTATTTCTAACTCGGTGCGACGAAATTTTCGTTGCAAG 120

Qy

923

CTCTTGAGCCCTTGAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAA 982

Db

121

CCCTTGAGATGCTTGAAATTTGGATGTCAAATAGATTCATATGCTAGTTGTCATCGTA 180

Qy

983

ACCGTGATGGAAGAGTGAACAAAGTGAAGCCCTGAAGCACTACAAATTTAGCTTAGCGT 1042

181 ACCGTGATGGCAAGTGGGCAAAAGTGGACACTTTTGAACGCTACAGATTCAGCTTGGCAT 240
1043 TTGAAAATTCGAATGAGGAGGATATGTAACCTGAAAAATTTCTTCCAATCCCTTGTGTGCTG 1102
241 TTGAGAAATTCATAGAGGAGGATACGTAACAGAAAAGTTTTCAGTCACTGGTAGCAG 300
1103 GAACTGCTGCTGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1162
301 GTTCTATTCCAGTTGTTGTGTGCTCCAAATATTCAAGAGATTTTCTCCGGGAGAGGTTG 360
1163 CAATTTTACATATAAGAGATAGAGGATGCTGAGTCTGTGCAAGAGACCATGAGATATC 1222
361 CAATATTACATATAAGAGAACCTTGATGATGCTTCAGTTGCTTAAGACAATGAATAA 420
1223 TAGCAGAAATCCCGAAGCATATAATCAATCAATGAGGTGGAGTATGAGGTGCCATCTG 1282
421 TTGCTCAATCTGATGCTTCAATCAATCTTTGAGGTGGAGTATGATGTCCTCTG 480
1283 ACTCTTCAAGCCCTTGTGGATATGCGAGCTGTGCAATCATCGTCCGCTTGTGCAATC 1342
481 ATTCTTTCAAGCCCTTATTGACATGCGAGCAGTTCATTCATCTTGTGCTTGTGTATAC 540
1343 ACTTGGCCAGCTGAGTAGAGAGAGAGAGAAATATCAAGCCTTAAGAGACGTCCTT 1402
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601 GTAGCTGTTCCAGAAAAGGAGACAGTTTACCACATATT 641

RESULT 15
CV534954
LOCUS
DEFINITION
NOD_210_G07 Phaseolus vulgaris nodule EST library Phaseolus
vulgaris cDNA 5', mRNA sequence.

CV534954
VERSION
KEYWORDS
SOURCE
ORGANISM
Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
1 (bases 1 to 599)
Ramirez,M., Graham,M.A., Blanco-Lopez,L., Silvente,S.,
Medrano-Soto,A., Blair,M.W., Hernandez,G., Vance,C.P. and Lara,M.
Sequencing and Analysis of Common Bean ESTs. Building a Foundation
for Functional Genomics
Plant Physiol. 137 (4), 1211-1227 (2005)
15824284
Contact: Blanco-Lara, L.
Nitrogen Fixation Centro
National Autonomous University of Mexico
Apartado Postal 565-A, Cuernavaca, Morelos, Mexico
Tel: 52 777 3291815
Email: blanco@cifn.unam.mx

Seq primer: T3.
FEATURES
source
1. .599
/organism="Phaseolus vulgaris"
/mol_type="mRNA"
/cultivar="Negro Jamaica 81"
/db_xref="taxon:3885"
/dev_stage="15 days post inoculation with Rhizobium
tropici CIAT 899"
/lab_host="SOLR"
/clone_lib="Phaseolus vulgaris nodule EST library"
/note="Organ: Nodules; Vector: pBluescript SK(+); Site_1:
EcoRI; Site_2: XhoI; Total RNA was prepared from P.
vulgaris nodules, 15 days post inoculation with Rhizobium
tropici CIAT 899. Poly (A+) RNA was obtained from total

RNA using oligo (dT) cellulose. Poly (A+) RNA was reverse
transcribed and cloned in the Uni-Zap XR vector
(Stratagene). Plasmids containing cDNAs were then excised
from the Uni- Zap XR vector and propagated in SOLR cells.
All sequences were searched for vector segments to check
for insert integrity. The sequences contain a minimum of
90 high quality bases and have been trimmed to remove
vector and adaptor sequences."

ORIGIN
Query Match 16.9%; Score 371; DB 7; Length 599;
Best Local Similarity 85.9%; Pred. No. 1.5e-86;
Matches 437; Conservative 0; Mismatches 65; Indels 7; Gaps 2;
QY 2 CTAATCTAAACGCTGATTTCTTTTCTTTCAGGGAACCATCCACCATTAACACAAA 61
DB 91 CTAATCTAAACGCTGCAATTTTCTCTTTTGGGAACCATCCACCATATAAGACAAC 150
QY 62 AAAAAACACAGC- ---AAGCTGTTTTTTTTTATCGTTCTTTTAAACAAAGCACCC 117
DB 151 AAAAAACACACATAAAGCTGTGTTTTTGTGTCATTTTTTCTTTAAACAGCACCCC 210
QY 118 CCATCATGGAATCGTCTCATAAACGCAAAATTTTCCATTTCCCTTTGATTTTATGTTA 177
DB 211 CCATCATGGAATCTGCTGCCATTAACGCCAAATTTATCCGTTTCCCTTTTATTTGTTT 270
QY 178 TTTTGGGAAATTGGCAGTTGGGGCGCAATTGAATGATGGGTCTGTGACGATCTTCGA 237
DB 271 TTTTGGGAAATTGGGAGTTGGAGGCGCAATCGAATGATGGGTCTGGTCAAGATCTTCGA 330
QY 238 GGCTCGAGAACAGATGGTCCCAACAAAGACAGCTTACCGTTTTTGGCTCCGGGAGCAAC 297
DB 331 GGTTCAAGAACAGAGGGTGCCCAACAAAGAGAGATGCCCGTTTTTGGCTCCGGTGGCAAC 390
QY 298 CCAAGAGGAAATGGAGCAATCTAATGCCTCTTTGTTGTTGCCCTTGTGTGTCATCGGGAG 357
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QY 358 ATCGCGTTTCTGGGTAGTTGGATATGGCCAAACCGCCCATGTTGACTCCCTCGCT 417
DB 451 ATCGCGTTTCTGGGTAGTTGGATATGGCCAAACCGCCCATGTTGACTCCCTCGCT 510
QY 418 GACTTCTTCTACCGCTCTCGAGCGTCTTGAAGGTGACGATTTGGGTTGGGT---TTG 474
DB 511 GACTTGTCTTACCGCTCTCTGTCGGTCTGTTGAAGGTGACGATTTGGGATGGGTGGTTG 570
475 GTGGCTTCTGATCGGAATTTCTGAATCGTA 503
571 GTGGCTTCTGATCGGAATTTCTGAATCGGA 599

Search completed: February 19, 2006, 18:14:06
Job time : 8812 secs